



(12) EUROPEAN PATENT APPLICATION

(43) Date of publication:
21.01.1998 Bulletin 1998/04

(51) Int. Cl.⁸: C12N 15/12, C12N 15/24,
A61K 48/00

(21) Application number: 97112154.6

(22) Date of filing: 16.07.1997

(84) Designated Contracting States:
AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC
NL PT SE
Designated Extension States:
AL LT LV RO SI

(72) Inventor:
Mixson, Archibald James
Rockville, MD 21201 (US)

(30) Priority: 16.07.1996 US 680845

(74) Representative:
Sieckmann, Raif, Dr. et al
Cohausz Hase Dawidowicz & Partner,
Patent- und Rechtsanwaltskanzlei,
Schumannstrasse 97
40237 Düsseldorf (DE)

(71) Applicant:
Mixson, Archibald James
Rockville, MD 21201 (US)

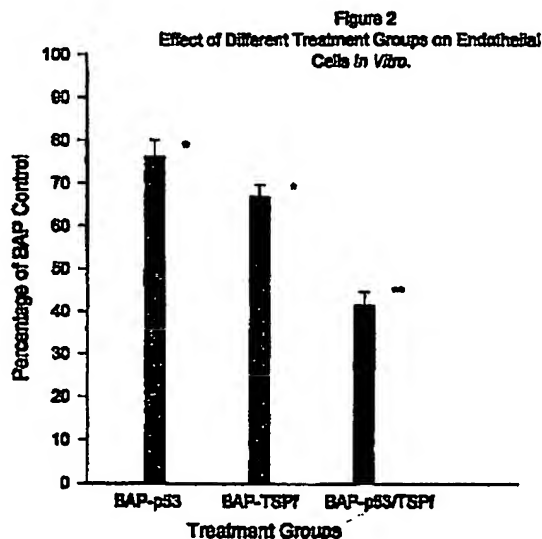
Remarks:

The applicant has subsequently filed a sequence
listing and declared, that it includes no new matter.

(54) Cationic vehicle: DNA complexes and their use in gene therapy

(57) Cationic vehicles: DNA complexes comprising
DNA encoding an anti-angiogenic peptide or DNA
encoding a tumor suppressor protein and DNA encod-

ing an anti-angiogenic peptide, as well as their use in
gene therapy, are disclosed.



*- BAP vs BAP-p53 or BAP-TSP1, $p < 0.05$

** - BAP-p53 or BAP-TSP1 vs BAP-p53/BAP-TSP1, $p < 0.01$

Description

FIELD OF THE INVENTION

5 The present invention relates to cationic vehicles DNA complexes (i.e. cationic liposome:DNA complexes, cationic polymer:DNA complexes) comprising DNA encoding an anti-angiogenic peptide, or DNA encoding a tumor suppressor protein and DNA encoding an anti-angiogenic peptide, and their use in gene therapy.

BACKGROUND OF THE INVENTION

10 1. Gene Therapy

Development of gene therapy techniques is approaching clinical realization for the treatment of neoplastic and metabolic diseases. The main obstacle in the treatment of malignant diseases, however, remains in the vector delivery system of the transgene to a distant target tissue.

Vectors carrying genes are commonly divided into viral and non-viral vector categories. Unfortunately, all vectors described to date have significant limitations. For example, replication-deficient retroviral vectors can efficiently transfect dividing cells. Local intratumoral injection of retroviruses that contain a thymidine kinase transgene has been used successfully to affect regression of gliomas (Cuiver et al, *Science*, 258:1550-1552 (1992)). However, retroviruses have the potential to cause insertional mutagenesis. As a result, their use has been limited to either direct injection of tumors or to ex vivo gene transfer trials. Unlike retroviral vectors, adenoviral vectors can also transfect non-dividing cells, and their ability to cause insertional mutagenesis is greatly reduced. However, they have the undesirable potential to activate the immune system in humans (Crystal, *Science*, 270:404-410, (1995)). Attempts are underway to minimize the immunogenicity of the adenoviral vectors, but the potential toxicity of viral vectors will most likely limit their use for systemic delivery of genes in the near future.

Non-viral vectors of DNA include liposomes, peptides, proteins and polymers (Ledley, *Current Opinion in Biotechnology*, 5:626-636 (1994)). Of these, liposomes are the most commonly used non-viral vectors of DNA. The major advantage of liposomes over retroviruses is that DNA is not incorporated into the genome, and unlike adenoviral vectors, they are not immunogenic. However, the major limitation of liposomes is that they are not as efficient as viral vectors in transfecting many cell types. Until recently, their medical utility was limited by their rapid uptake by phagocytic cells. Interest in liposomes as a vector was rejuvenated by two technological advances that have produced a renaissance in the field. First, sterically stabilized (Stealth) liposomes represent a significant breakthrough in that they are non-reactive, and are not readily taken up by the reticuloendothelial system (RES). Stealth liposomes are composed of lipids rich in oxygen in their head group (ethylene glycol or glycolipids) which provide a steric barrier outside of the membrane. As a result, Stealth liposomes remain in the blood for up to 100 times longer than conventional liposomes, and can thus increase pharmacological efficacy (Papahadjopoulos, In: *Stealth liposomes*, Ed., Lasic et al, CRC Press (1995); and Lasic et al, *Science*, 267:1275-76 (1995)). However, Stealth liposomes are still not particularly efficient in transfection of cells or as vectors for DNA.

The second significant advance in liposome technology has been the use of cationic liposomes complexed to negatively-charged DNA. Cationic liposomes can condense DNA, and increase transfection yields several orders of magnitude. In the cationic liposome:DNA complex, the nucleic acids or oligonucleotides are not encapsulated, but are simply complexed with small unilamellar vesicles by electrostatic interactions. The exact nature of the cationic liposome:DNA complex is not clear, but intricate topological rearrangements of the cationic liposome:DNA complex occur, including DNA condensation, liposome aggregation, and fusion. This supramolecular complex can be added to cells in vitro, injected parenterally, or aerosolized for pulmonary applications (Lasic et al, *Science*, 267:1275-1278 (1995)). Further, the intravenous injection into mice of high concentrations of the CAT gene (100 µg or greater) complexed with cationic liposomes has been found to result in 40% transfection efficiency of well vascularized tissues, such as the spleen (Zhu et al, *Science*, 261:209-211 (1993)). However, a major challenge of gene therapy remains the systemic delivery of transgenes to the tumor or peritumoral area that will effectively decrease the size of primary tumors and their metastases. This is because unlike the spleen and bone marrow, which are highly vascular and have a high capacity to filter macromolecules from the blood stream, most organs and tumors do not have this capacity, and the transfection efficiency of these tissues with liposomes is low (Marshall, *Science*, 269:1051-1055 (1995)). In addition, another limitation of cationic liposome: DNA complexes is that their 1/2 life in the blood stream is less than one hour (Allen et al, In: *Liposome Technology-Vol. III*, Ed., Gregoriadis G et al, CRC Press (1993)). Sufficient transfection of the target cell by vectors carrying therapeutic genes has thus far been the rate-limiting step in gene therapy.

II. Tumor Suppressor Genes

Tumor suppressor genes are well-known in the art, and include the p53 gene (Baker et al, *Science*, 249:912-915 (1990)), the p21 gene (El-Deiry et al, *Cell*, 75:817-825 (1993); and Harper et al, *Cell*, 75:805-816 (1993)), and the rb gene (Bookstein et al, *Science*, 247:712-715 (1990)).

Mutations in the tumor suppressor gene p53 are known to occur in over 50% of human tumors, including metastatic breast cancer (Vogelstein, *Nature*, 348:681-682 (1990)). Breast cancer is one of the leading causes of death in women in North America and Western Europe, affecting nearly 10% of this population living to 80 years of age, and one million new cases are predicted by the end of this decade (Miller et al, *Int. J. Cancer*, 37:173-177 (1986)). Although the molecular basis of multistage carcinogenesis in breast cancer is not well understood, the metastatic potential of breast cancers has been correlated with the presence of point mutations in the p53 gene (Wang et al, *Oncogene*, 8:279-288 (1993)). Various groups have found that reintroduction of the wild-type P53 into a tumor cell has the therapeutic potential to inactivate the proliferative effects of the mutated product (Bookstein et al, *Cancer*, 71:1179-1186 (1993); Chen et al, *Science*, 250:1578-1580 (1990); and Baker et al, *Science*, 249:912-915 (1990)). For example, *in vitro* transfection and retroviral-mediated transfer of a single copy of the p53 transgene into a variety of tumor cells, including breast cancer cells, was found to result in a decrease in growth rate and/or attenuated tumor development once those transfected cells were implanted into nude mice (Wang et al, *Oncogene*, 8:279-288 (1993); Baker et al, *Science*, 249:912-915 (1990)); Bookstein et al, *Science*, 247:712-715 (1990); Cheng et al, *Cancer Res.*, 52:222-226 (1992); Isaacs et al, *Cancer Res.*, 51:4716-4720 (1991); Diller et al, *Mol. Cell. Biol.*, 10:5772-5781 (1990); Chen et al, *Oncogene*, 6:1799-1805 (1991); and Zou et al, *Science*, 263:528-529 (1994)). In addition, intratracheal injection of a retrovirus containing the p53 transgene has been shown to significantly inhibit the growth of lung tumors (Fujiwara et al, *J. Natl. Cancer Inst.*, 88:1458-1462 (1994)). Further, systemic intravenous administration of a β -actin promoter-containing vector containing the p53 coding sequence complexed to cationic liposomes has been found to affect the tumor growth of a malignant line of breast cancer cells injected into nude mice (Lesoon-Wood et al, *Proc. Am. Ass. Cancer Res.*, 38:421 (1995); and Lesoon-Wood et al, *Human Gene Ther.*, 6:39-406 (1995)). Of the 15 tumors treated in this study, four of these tumors did not respond to treatment. Because of the unresponsiveness of these tumors, new therapies were sought in the present invention to more effectively decrease the size of these tumors. Based on the *in vitro* data concerning p53, one might expect that p53 decreases the size of the tumors due to efficient transfection of the tumor. However, less than 5% of the tumor was transfected after three injections of a cationic liposome:marker (CAT) gene. Furthermore, some endothelial cells of the tumor were transfected with this marker gene. Thus, the primary target of cationic liposome:p53 complex may be the vasculature system of the tumor. Given that angiogenesis is critical for the development of any human tumor, as well as for metastases (Fidler et al, *Cell*, 79:185-188 (1994)), this therapy should be widely applicable to a wide variety of tumors.

p53 coordinates multiple responses to DNA damage. DNA damage results in an increase in the level of the p53 protein. Following DNA damage, an important function of wild-type p53 function is to control the progression of cells from G1 to S phase. Recently, several groups have found that p53 transcriptionally activates a p21 kd protein (also known as WAF1 or Cip1), an inhibitor of cyclin-dependent kinases (CDKs) (El-Deiry et al, *supra*; and Harper et al, *supra*). Inhibition of CDK activity is thought to block the release of the transcription factor E2F, and related transcription factors from the retinoblastoma protein RB, with consequent failure to activate transcription of genes required for S phase entry (Harper et al, *supra*; and Xiong et al, *Nature*, 366:701-704 (1993)). Evidence consistent with the model that pRb is a downstream effector of p53-induced G1 arrest has recently been reported (Dulic et al, *Cell*, 78:1013-1023 (1994)). Thus, p53 regulates cell cycle through two proteins: p21 and rb.

III. Anti-Angiogenic Proteins

Proteins with anti-angiogenic activities are well-known and include: thrombospondin I (Kostfeld et al, *J. Biol. Chem.*, 267:18230-18238 (1993); Tolma et al, *J. Cell Biol.*, 122:497-511 (1993); and Dameron et al, *Science*, 265:1582-1584 (1995)), IL-12 (Voest et al, *J. Natl. Cancer Inst.*, 87:581-588 (1995)), protamine (Ingber et al, *Nature*, 348:555-557 (1990)), angiostatin (O'Reilly et al, *Cell*, 79:315-328 (1994)), laminin (Sakamoto et al, *Cancer Res.*, 5:903-906 (1991)), and a prolactin fragment (Clapp et al, *Endocrinol.*, 133:1292-1299 (1993)). In addition, several anti-angiogenic peptides have been isolated from these proteins (Malone et al, *Science*, 247:77-79 (1990); Weiering et al, *J. Surg. Res.*, 50:245-251 (1991); and Eljan et al, *Mol. Biother.*, 3:38-40 (1991)).

Thrombospondin I (hereinafter "TSPI") is a large trimeric glycoprotein composed of three identical 180 kd subunits (Lahav et al, *Semin. Thromb. Hemostasis*, 13:352-360 (1987)) linked by disulfide bonds (Lawer et al, *J. Cell Biol.*, 103:1635-1648 (1986); and Lahav et al, *Eur. J. Biochem.*, 145:151-156 (1984)). The majority of anti-angiogenic activity is found in the central stalk region of this protein (Tolma et al, *supra*). There are at least two different structural domains within this central stalk region that inhibit neovascularization (Tolma et al, *supra*).

Besides TSPI, there are five other proteins (fibronectin, laminin, platelet factor-4, angiostatin, and prolactin frag-

ment) in which peptides have been isolated that inhibit angiogenesis. In addition, analogues of the peptide somatostatin are known to inhibit angiogenesis.

Fibronectin (FN) is a major surface component of many normal cells, as well as a potent cell spreading factor. During transformation, the loss of cellular FN has been observed. Furthermore, the addition of fibronectin to transformed cells restores the normal phenotype. It has been found that either heparin-binding or cell-adhesion fragments from FN can inhibit experimental metastasis, suggesting that cell surface proteoglycans are important in mediating the adhesion of metastatic tumor cells (McCarthy et al, *J. Natl. Cancer Inst.*, 80:108-116 (1988)). It has also been found that FN and one of its peptides inhibits *in vivo* angiogenesis (Eijan et al, *Mol. Biother.*, 3:38-40 (1991)).

Laminin is a major component of the basement membrane, and is known to have several biologically active sites that bind to endothelial and tumor cells. Laminin is a cruciform molecule that is composed of three chains, an A Chain and two B chains. Several sites in laminin have been identified as cell binding domains. These sites promote cellular activities *in vitro*, such as cell spreading, migration, and cell differentiation. Two peptides from two sites of the laminin B1 chain are known to inhibit angiogenesis (Grant et al, *Path. Res. Pract.*, 190:854-863 (1994)).

Platelet factor-4 (PF4) is a platelet α -granule protein originally characterized by its high affinity for heparin. The protein is released from platelets during aggregation as a high molecular weight complex of a tetramer of the PF4 polypeptide and chondroitin sulfate, which dissociates at high ionic strength. PF4 has several biological properties including immunosuppression, chemotactic activity for neutrophils and monocytes as well as for fibroblasts, inhibition of bone resorption, and inhibition of angiogenesis. The angiostatic properties of human PF4 are associated with the carboxyl-terminal, heparin binding region of the molecule. A 12 amino acid synthetic peptide derived therefrom has been discovered to have marked angiostatic effects (Maione et al, *Science*, 247:77-79 (1990)).

Although somatostatin is not a protein, it is a naturally-occurring cyclic 14 amino acid peptide whose most-recognized function is the inhibition of growth hormone (GH) secretion. Somatostatin is widely distributed in the brain, in which it fulfills a neuromodulatory role, and in several organs of the gastrointestinal tract, where it can act as a paracrine factor or as a true circulating factor. The role played by the neuropeptide somatostatin, also known as somatotropin release inhibitory factor (SRIF), in human cancer is not well understood. Recent investigations involving somatostatin receptors in normal and neoplastic human tissues suggest that the action is complex, and involves both direct and indirect mechanisms. One of the anti-tumor mechanisms of these synthetic somatostatin analogues may be an anti-angiogenic effect (Woltering et al, *J. Surg. Res.*, 50:245-50 (1990)). In a recent study, the ability of native somatostatin and nine somatostatin analogues to inhibit angiogenesis were evaluated. The most potent somatostatin analogue was found to be approximately twice as potent as the naturally-occurring somatostatin (Barrie et al, *J. Surg. Res.*, 55:446-50 (1993)).

Angiostatin is a 38 kDa polypeptide fragment of plasminogen. Whereas plasminogen has no fibrinogenic activity, angiostatin has marked angiogenic activity (O'Reilly MS, et al *Cell*, 79:315-28 (1994)). Angiostatin was isolated when it was observed that the primary tumor suppressed metastases. That is, when the primary tumor was removed, the metastases grew. Administration of angiostatin blocks neo-vascularization and growth of metastases.

Finally, a 16kd fragment of prolactin has been found to be angiogenic. Similar to plasminogen, prolactin is not anti-angiogenic but the prolactin fragment is a potent *in vivo* and *in vitro* inhibitor of angiogenesis (Clapp C. et al. *Endocrinology*. 133:1292-1299 (1993)).

Despite the evidence that anti-angiogenic peptides are effective anti-tumor agents, as well as the great deal of interest in targeting genes toward the vasculature, there have been no published reports on effective *in vivo* gene therapy regimens with established anti-angiogenic DNA sequences.

There are several reasons why gene therapy utilizing antiangiogenic genes have not been used or why antiangiogenic peptides are effective and the liposome: antiangiogenic gene may not be. First, there are significant physical differences between the liposome: DNA complexes and their peptides. Cationic liposomes have a 1/2 life of less than one hour (Allen TM and Papahadjopoulos D, In: *Liposome Technology-Vol. III*, Ed., Gregoriadis G et al, CRC Press (1993)), whereas the most effective of the antiangiogenic peptides (i.e angiostatin) have a 1/2 life of two days (Folkman J, The John Krantz, Jr Lecture in Pharmacology, UMAB, 4/30/96). Since cationic liposomes form large aggregates when mixed with DNA, the distribution of these complexes is likely to be quite different from the much smaller peptides (need reference). These properties of the liposomes may account for the low transfection efficiency of a tumor. Therefore, it is uncertain as to whether these liposome:DNA complexes will reach their cellular targets.

Furthermore, the exact receptor target or mechanisms of these antiangiogenic peptides are unknown (Tolsma et al, *supra*). For example, it is unknown whether these receptor targets are intracellular or extracellular. The anti-angiogenic genes that are complexed to liposomes encode their respective proteins inside the cell, and proteins without secretory sequences remain inside the cell. Thus, it is unclear that a intracellular antiangiogenic peptide derived from a systemically transfected gene will reach its cellular and/or receptor target.

The only transfected antiangiogenic gene that has inhibited tumor growth is full length thrombospondin I. In this study (Weinstat-Saskow et al, *Cancer Research* 54, 6504-6511, (1994)) tumor cells that expressed 15 fold higher levels of the thrombospondin I *in vitro* than baseline cells were implanted into the mice. This transfected full length throm-

bospondin I was secreted from the tumor cells to inhibit angiogenesis, and effectively reduced the tumor by 60%. Thus, this study determined that transfection of 100% of the tumor cells with a highly expressed secreted antiangiogenic gene was able to reduce tumor size.

6 SUMMARY OF THE INVENTION

An object of the present invention is to provide cationic vehicles:DNA complexes, such as liposome complexes containing DNA encoding anti-angiogenic peptides or cationic complexes containing DNA encoding an anti-angiogenic peptides.

10 Another object of the present invention is to provide a method of anti-angiogenic gene therapy.

Still another object of the present invention is to provide liposome complexes containing DNA encoding an anti-angiogenic peptide.

Yet another object of the present invention is to provide liposome complexes containing DNA encoding an anti-angiogenic peptide in combination with DNA encoding a tumor suppressor gene.

15 A further object of the present invention is to provide liposome complexes containing DNA encoding concatamers of the same or different anti-angiogenic peptides.

An additional object of the present invention is to provide a method for inhibiting tumor growth in a subject, or alternatively, to use these complexes for the production of a medicament, especially for inhibiting tumor growth in a subject.

20 These and other objects of the present invention, which will be apparent from the detailed description of the invention provided hereinafter, have been met in one embodiment, by a cationic liposome:DNA complex comprising DNA encoding an anti-angiogenic peptide and DNA encoding a tumor suppressor protein.

Further objects of the present invention were solved by the features defined in the present set of claims, but especially the preferred embodiments defined in claims 2 to 25.

25 Based on the present invention, it is anticipated that one skilled in the gene therapy could utilize other cationic carriers (polylysine, polyhistidine, polycat57, Superfect, and polyethylimine) complexed with the antiangiogenic genes to inhibit tumors.

DETAILED DESCRIPTION OF THE INVENTION

30 As discussed above, in one embodiment, the above-described objects of the present invention have been met by a non-viral:DNA complex comprising DNA encoding an anti-angiogenic peptide and DNA encoding a tumor suppressor protein.

The particular non-viral carrier (liposomes-neutral or non-cationic, see below), polyethylimine (Fluka), polylysine (Sigma), polyhistidine (Sigma), Superfect (Qiagen), are not critical to the present invention although cationic liposomes are preferable carriers. Examples of cationic lipids which can be employed in the present invention include include 1,2-dioleoyl-sn-glycero-3-ethylphosphocholine (Avanti, Birmingham, AL), 1,2-dimyristoyl-sn-glycero-3-ethylphosphocholine (Avanti, Birmingham, AL), and (2,3-di-*o*-octyloxy)propyl-N,N,N-trimethylammonium chloride (DOTMA) (Syntex Corp., Palo Alto, CA).

40 The cationic lipids are preferably used in a mixture with dioleoylphosphatidylethanolamine (DOPE) (Avanti, Birmingham, AL). In the present invention, the amount of cationic lipid present in the mixture is generally in the range of from 100% to 40% (w/w), preferably about 50% (w/w); and the amount of DOPE present in the mixture is generally in the range of from 0% to 60% (w/w), preferably about 50% (w/w); and the amount of pegylated lipid (1,2-diacyl-sn-glycero-3-phosphoethanolamine-N-[Poly(ethylene glycol) 2000] present in the mixture is generally in the range of from 0% to 10% (w/w), preferably about 1% (w/w).

45 The particular ligand will be dependent on the the tumor/peritumoral targeted. Examples of targets on tumors include Her2 (breast), CEA (colon), ferritin receptor (breast, lung, and ovary), and the tumor vasculature (α vB3 integrins or tissue factor). Antibodies directed toward Her2, CEA, and the tumor's vasculature will be coupled to 1% of the pegylated lipid hydroxyl group of the pegylated lipid with a water soluble carbodiimide (1-ethyl-3-(3-dimethylamino-propyl) carbodiimide), and purified over a sepharose CL-6B column. Similarly, ligands to the tumor (ferritin) and/or the vasculature (the peptide, RGD) are covalently attached to the hydroxyl the pegylated lipids.

50 The particular tumor suppressor gene employed is not critical to the present invention. Examples of such tumor suppressor genes include the p53 gene, the p21 gene (El-Deiry et al, *supra*; and Harper, *supra*), and the rb gene (Bookstein et al, *supra*). The p53 gene is the preferred tumor suppressor gene employed in the present invention.

55 The particular anti-angiogenic peptide encoded by the DNA is not critical to the present invention. Examples of said peptides include a fragment of thrombospondin I (TSP1) having the following amino acid sequence (the amino acid sequences that are known to be anti-angiogenic are underlined):

MTEENKELANELRRPPLCYHNGVQYRNNEEWTVDSCTECHCQNSVTICKKVSCP
 5 IMPCSNATVPDGECCPRCWP SDSADDGWSPWSEWTSCSTSCGNGIQQRGRSCDS
 LNNRCEGSSVQTRTCHI QEC DKRFKQDGGW SHWSPWSSCSVT CGDGVITRITLC
 NSPSPQMNGKPCEGEARETKACKKDACP INGGWGPWSPWDICSVTCGGGVQKRS
 10 RL (SEQ ID NO:1),

which is encoded by the following DNA sequence (nucleotides 1013-1650 of the TSP1 gene; the underlined sequences encode the anti-angiogenic peptides; the bold TAA is the stop codon):

15 ATGACTGAAGAGAACAAAGAGTTGGCCAATGAGCTGAGGCGGCCTCCCCCT
ATGCTATCACAACGGAGTTCAGTA CAGAAATAACGAGGAATGGACTGTTG
 ATAGCTGCACTGAGTGTCACTGTCAGAACTCAGTTACCATCTGCAAAAAG
 20 GTGTCCTGCCCATCATGCCCTGCTCCAATGCCACAGTTCTTGATGGAGA
 ATGCTGTCCTCGCTGTTGGCCCAGCGACTCTGCGGACGATGGCTGGTCTC
 CATGGTCCGAGTGGACCTCCTGTTCTACGAGCTGTGGCAATGGAATTGAG
 25 CAGCGCGGCCGCTCCTGCGATAGCCTCAACAACCGATGTGAGGGCTCCTC
 GGTCCAGACACGGACCTGCCACATTCAGGAGTGTGACAAAAGATTTAAC
 AGGATGGTGGCTGGAGCCACTGGTCCCCGTTGGTCATCTTGTCTGTGACA
 30 TGTGGTGATGGTGTGATCACAAAGGATCCGGCTCTGCAACTCTCCAGCCC
 CCAGATGAATGGGAAACCCTGTGAAGGCGAAGCGCGGGAGACCAAAGCCT
 GCAAGAAAGACGCCTGCCCATCAATGGAGGCTGGGGTCTTGGTCACCA
 35 TGGGACATCTGTTCTGTACCTGTGGAGGAGGGGTACAGAAACGTAGTCT
 CTCTAA (SEQ ID NO:2);

a concatamer of TSP1 having the following amino acid sequence (the intervening sequence is underlined):

40 MTEENKELANELRRPPLCYHNGVQYRNNEEWTVDSCTECHCQNSVTICKKVSCP
 IMPCSNATVPDGECCPRCWP SDSADDGWSPWSEWTSCSTSCGNGIQQRGRSCDS
 45 LNNRCEGSSVQTRTCHI QEC DKRFKQDGGW SHWSPWSSCSVT CGDGVITRITLC
 NSPSPQMNGKPCEGEARETKACKKDACP INGGWGPWSPWDICSVTCGGGVQKRS
 50
 55

RLCVHSRMTEENKELANELRRPPLCYHNGVQYRNNEEWTVDSCTECHCQNSVTI
 CKKVSCPIMPSCNATVPDGECCPRCWPSDSADDGWSFWSEWTSCSTSCGNGIQQ
 6 RGRSCDSLNNRCEGSSVQTRTCHIQECDKRFKQDGGWSHWSFWSSCSVTCDGV
 ITRIITLNSPSPQMNKGKPCGEARETKACKKDACPINGGWGPWSPWDICSVTCG
 GGVQKRSRL (SEQ ID NO:3),

10 which is encoded by the following DNA sequence (the intervening sequence is underlined):

ATGACTGAAGAGAACAAAGAGTTGGCCAATGAGCTGAGGCGGCCTCCCC
 15 TATGCTATCACAACGGAGTTCAGTACAGAAATAACGAGGAATGGACTGTT
 GATAGCTGCACTGAGTGTCACTGTGAGAACTCAGTTACCATCTGCAAAA
 GGTGTCCTGCCCCATCATGCCCTGCTCCAATGCCACAGTTCCTGATGGAG
 20 AATGCTGTCTCGCTGTTGGCCAGCGACTCTGCGGACGATGGCTGGTCT
 CCATGGTCCGAGTGGACCTCCTGTTCTACGAGCTGTGGCAATGGAATTCA
 GCAGCGCGGCCGCTCCTGCGATAGCCTCAACAACCGATGTGAGGGCTCCT
 CGGTCCAGACACGGACCTGCCACATTGAGGAGTGTGACAAAAGATTAA
 25 CAGGATGGTGGCTGGAGCCACTGGTCCCCGTGGTCATCTTGTTCTGTGAC
 ATGTGGTGATGGTGTGATCACAAGGATCCGGCTCTGCAACTCTCCAGCC
 CCCAGATGAATGGGAAACCTGTGAAGGCGAAGCGCGGGAGACCAAAGCC
 30 TGCAAGAAAGACGCCTGCCCCATCAATGGAGGCTGGGGTCCTTGGTCACC
 ATGGGACATCTGTTCTGTACCTGTGGAGGAGGGGTACAGAAACGTAGTC
 GTCTCTGCGTCGACTCTAGAATGACTGAAGAGAACAAAGAGTTGGCCAA
 35 TGAGCTGAGGCGGCCTCCCCATGCTATCACAACGGAGTTCAGTACAGAA
 ATAACGAGGAATGGACTGTTGATAGCTGCACTGAGTGTCACTGTCAGAAC
 TCAGTTACCATCTGCAAAAAGGTGTCCTGCCCCATCATGCCCTGCTCCAA
 40 TGCCACAGTTCCTGATGGAGAATGCTGTCTCGCTGTTGGCCAGCGACT
 CTGCGGACGATGGCTGGTCTCCATGGTCCGAGTGGACCTCCTGTTCTACG
 AGCTGTGGCAATGGAATTCAGCAGCGCGGCCGCTCCTGCGATAGCCTCAA
 45 CAACCGATGTGAGGGCTCCTCGGTCCAGACACGGACCTGCCACATTCAGG
 AGTGTGACAAAAGATTAAACAGGATGGTGGCTGGAGCCACTGGTCCCCG
 TGGTCATCTTGTTCTGTGACATGTGGTGATGGTGTGATCACAAGGATCCG
 50 GCTCTGCAACTCTCCAGCCCCAGATGAATGGGAAACCTGTGAAGGCG
 AAGCGCGGGAGACCAAAGCCTGCAAGAAAGACGCCTGCCCCATCAATGGA
 GGCTGGGGTCCTTGGTCACCATGGGACATCTGTTCTGTACCTGTGGAGG
 55 AGGGGTACAGAAACGTAGTCGTCTCTAA (SEQ ID NO:4);

laminin peptide having the following amino acid sequence: MYIGSR (SEQ ID NO:5), which is encoded by the following

DNA sequence (the *Sa*I sites are underlined, and the stop codon is in bold):

GTCGACATGTATATTGGTTCTCGTTAAGTCGAC (SEQ ID NO:8);

a concatamer of the laminin sequence having the following amino acid sequence (the intervening sequences are underlined):

6 MYIGSRGKSYIGSRGKSYIGSRGKS (SEQ ID NO:7), which is encoded by the following DNA sequence (the *Sa*I sites are underlined, and the intervening sequences are in bold):

GTCGACATGTATATTGGTTCTCGTGGTAAAAGATATATTGGTTCTCGTGGTAAA

10 AGATATATTGGTTCTCGTGGTAAAAGATAAGTCGACC (SEQ ID NO:8);

a peptide from platelet factor-4 having the following amino acid sequence:

MLYKKIKKLLLES (SEQ ID NO:9), which is encoded by the following DNA sequence (the *Sa*I sites are underlined):

16 GTCGACATGCTTTATAAGAAGATCATCAAGAAGCTTCTTGAGAGTTAAGTCGAC (SEQ ID NO:10);

a concatamer of the platelet factor-4 peptide having the following amino acid sequence (the intervening sequences are underlined):

MLYKKIKKLLLESQKSLYKKIKKLLLESQKSLYKKIKKLLLESQKS (SEQ ID NO:11), which is encoded by the following DNA sequence (the *Sa*I sites are underlined, and the intervening sequences are in bold):

20 GTCGACATGCTTTATAAGAAGATCATCAAGAAGCTTCTTGAGAGTGGTAAAAGA

CTTTATAAGAAGATCATCAAGAAGCTTCTTGAGAGTGGTAAAAGACTTTATAAG

26 AAGATCATCAAGAAGCTTCTTGAGAGTGGTAAAAGATAAGTCGAC (SEQ ID NO:12);

somatostatin inhibitor having the following amino acid sequence: MFCYWKVCW (SEQ ID NO:13), which is encoded by the following DNA sequence (the *Sa*I sites are underlined):

30 GTCGACATGTTCTTGTATTGGAAGGGATTGTGGTAAATCGAC (SEQ ID NO:14);

a concatamer of somatostatin inhibitor having the following amino acid sequence (the intervening sequences are underlined):

35 MFCYWKVCWQKSFYWKVCWQKSFYWKVCWQKS (SEQ ID NO:15), which is encoded by the following DNA sequence (the *Sa*I sites are underlined, and the intervening sequences are in bold):

GTCGACATGTTCTTGTATTGGAAGGGATTGTGGGGTAAAAGATTCTTGTATTGG

40 AAGGGATTGTGGGGTAAAAGATTCTTGTATTGGAAGGGATTGTGGGGTAAAAGA

TAAGTCGAC (SEQ ID NO:16);

fibronectin inhibitor having the following amino acid sequence: MGRGD (SEQ ID NO:17), which is encoded by the following DNA sequence (the *Sa*I sites are underlined):

45 GTCGACATGTTCTTGTATTGGAAGACTTTGACTTAAATCGAC (SEQ ID NO:18);

a concatamer of fibronectin inhibitor having the following amino acid sequence (the intervening sequences are underlined):

50 MGRGDQKSGRGDQKSGRGDQKS (SEQ ID NO:19); which is encoded by the following DNA sequence (the *Sa*I sites are underlined, and the intervening sequences are in bold):

GTCGACATGGGTCGTGGTGATGGTAAAAGAGGTCGTGGTGATGGTAAAAGA
 GGTTCGTGGTGATGGTAAAAGATAAGTCGAC (SEQ ID NO:20);
 angiotstatin having the following amino acid sequence:
 MVYLSECKTGIGNGYRGTMSTRKSGVACQKWGATFFHVPNYSPSTHPNEGLEEN
 YCRNPDNDEQGFWCYTTDPDKRYDYCNIPCEEEECMYCSGEKYEKISKTMMSG
 LDCQAWDSQSPHAGYIPAKTFPSKNLKMNYCHNPDGEPRPWCFTTDPTRWEYC
 DIPRCTTPPPPPSPPTYQCLKGRGENYRGTVSVTVSGKTCQRWSEQTPHRHNRTP
 ENFPCKNLEENYCRNPDGETAPWCYTTSQRLRWEYCEIPSCCESSASPDQSDSSV
 PFEEQTFVVQECYQSDGQSYRGTSSTTTTGKKCQSEQTPHR
 (SEQ ID NO:21),

which is encoded by the following DNA sequence (the *Sa*I sites are underlined):

GTCGACATGGTGTATCTGTCAGAATGTAAGACCGGCATCGGCAACGGC
 TACAGAGGAACCATGTCCAGGACAAAGAGTGGTGTGCCTGTCAAAG
 TGGGGTGCCACGTTCCCCACGTACCCAACTACTCTCCAGTACACAT
 CCCAATGAGGGACTAGAAGAGAACTACTGTAGGAACCCAGACAATGAT
 GAACAAGGGCCTTGGTGCTACACTACAGATCCGGACAAGAGATATGAC
 TACTGCAACATTCCCTGAATGTGAAGAGGAATGCATGTACTGCAGTGGA
 GAAAAGTATGAGGGGAAAATCTCCAAGACCATGTCTGGACTTGACTGC
 CAGGCCTGGGATTCTCAGAGCCCATGCTCATGGATACATCCCTGCC
 AAATTTCCAAGCAAGAACCTGAAGATGAATTATTGCCACAACCCTGAC
 GGGGAGCCAAGGCCCTGGTGCTTCAACACAGACCCACCAAACGCTGG
 GAATACTGTGACATCCCCCGCTGCACAACACCCCGCCCCACCCAGC
 CCAACCTACCAATGTCTGAAAGGAAGAGGTGAAAATTACCGAGGGACC
 GTGTCTGTACCGTGTCTGGGAAAACCTGTCAGCGCTGGAGTGAGCAA
 ACCCCTCATAGGTGA GTCGAC (SEQ ID NO:22),

a concatamer of angiotstatin having the following amino acid sequence (the intervening sequences are underlined):

6
10
14
18
20
MVYLSECKTGIGNGYRGTMSTRKSGVACQKWGATFPHVPNYSPSTHPNEGLE
ENYCRNPDNDEQGPWCYTTPDKRYDYCNIPCEEEECMYCSGEKYEKISKMTMS
GLDCQAWDSQSPHAHGYIPAKFPSKNLKMNYCHNPDGEPRPWCFTTDP TKRWEY
CDIPRCTTPPPPPSPTYQCLKGRGENYRGTVSVTVSGKTCQRWSEQTPHRHNRT
PENFPCKNLEENYCRNPDGETAPWCYTTPDSQLRWEYCEIPSCCESSASPDQSDSS
VPPEEQTPVVQECYQSDGQSYRGTSSTTITGKKCQSEQTPHRGKSMVYLSECKT
GIGNGYRGTMSTRKSGVACQKWGATFPHVPNYSPSTHPNEGLEENYCRNPDNDE
QGPWCYTTPDKRYDYCNIPCEEEECMYCSGEKYEKISKMTMSGLDCQAWDSQS
PHAHGYIPAKFPSKNLKMNYCHNPDGEPRPWCFTTDP TKRWEYCDIPRCTTPPP
PPSPTYQCLKGRGENYRGTVSVTVSGKTCQRWSEQTPHRHNRTPENFPCKNLEE
NYCRNPDGETAPWCYTTPDSQLRWEYCEIPSCCESSASPDQSDSSVPPEEQTPVVQ
ECYQSDGQSYRGTSSTTITGKKCQSEQTPHR (SEQ ID No :23),

which is encoded by the following DNA sequence (the *Sa*I sites are underlined, and the intervening sequences are in bold):

25
30
35
40
45
50
55
GTCGACATGGTGTATCTGTCAGAATGTAAGACCGGCATCGGCAACGGCTACA
GAGGAACCATGTCCAGGACAAAGAGTGGTGTTCCTGTCAAAGTGGGGTGC
CACGTTCCCCACGTACCCAACACTCTCCCAGTACACATCCCAATGAGGGA
CTAGAAGAGAACTACTGTAGGAACCCAGACAATGATGAACAAGGGCCTTGGT

5 GCTACACTACAGATCCGGACAAGAGATATGACTACTGCAACATTCCCTGAATG
 TGAAGAGGAATGCATGTACTGCAGTGGAGAAAAGTATGAGGGCAAATCTCC
 AAGACCATGTCTGGACTTGACTGCCAGGCCTGGGATTCTCAGAGCCCACATG
 CTCATGGATACATCCCTGCCAAATTTCCAAGCAAGAACCTGAAGATGAATTA
 10 TTGCCACAACCTTGACGGGGAGCCAAGGCCCTGGTGCTTCACAACAGACCCC
 ACCAAACGCTGGGAATACTGTGACATCCCCCGCTGCACAACACCCCGCCCC
 CACCCAGCCCCAACCTACCAATGTCTGAAAGGAAGAGGTGAAAATTACCGAGG
 GACCGTGTCTGTCAACGTGTCTGGGAAAACCTGTCAGCGCTGGAGTGAGCAA
 15 ACCCCTCATAGGGGTAAAAGAATGGTGTATCTGTCAGAATGTAAGACCGGCA
 TCGGCAACGGCTACAGAGGAACCATGTCCAGGACAAAGAGTGGTGTTCCTG
 TCAAAGTGGGGTGCCACGTTCACCCACGTACCCAACCTACTCTCCAGTACA
 20 CATCCCAATGAGGGACTAGAAGAGAACTACTGTAGGAACCCAGACAATGATG
 AACAAGGGCCTTGGTGCTACACTACAGATCCGGACAAGAGATATGACTACTG
 CAACATTCCCTGAATGTGAAGAGGAATGCATGTACTGCAGTGGAGAAAAGTAT
 25 GAGGGCAAATCTCCAAGACCATGTCTGGACTTGACTGCCAGGCCTGGGATT
 CTCAGAGCCCACATGCTCATGGATACATCCCTGCCAAATTTCCAAGCAAGAA
 CCTGAAGATGAATTATTGCCACAACCTTGACGGGGAGCCAAGGCCCTGGTGCT
 30 TCACAACAGACCCCAACCAACGCTGGGAATACTGTGACATCCCCCGCTGCACAA
 CACCCCGCCCCCACCAGCCCCAACCTACCAATGTCTGAAAGGAAGAGGTGAAA
 ATTACCGAGGGACCGTGTCTGTCAACGTGTCTGGGAAAACCTGTCAGCGCTGGA
 35 GTGAGCAA ACCCCTCATAGGTGA GTCGAC (SEQ ID NO:24);

prolactin having the following amino acid sequence:

40 MLPICPGGAARQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFI
 TKAINSCHTSSLATPEDKEQAQOMNQKDFLSLIVSILRSWNEPLYHLVTEVR
 GMQEAPAILSKAVEIEEQTK (SEQ ID NO:25),

48 which is encoded by the following DNA sequence:
 50
 55

ATGTTGCCCATCTGTCCCGCGGGGCTGCCCGATGCCAGGTGACCCCTTCGAG
 ACCTGTTTGACCGCGCCGTCGTCTGTCCCACTACATCCATAACCTCTCCTC
 5 AGAAATGTTTCAGCGAATTCGATAAACGGTATACCCATGGCCGGGGGTTTCATT
 ACCAAGGCCATCAACAGCTGCCACACTTCTTCCCTTGCCACCCCGAAGACA
 AGGAGCAAGCCCAACAGATGAATCAAAAAGACTTTCTGAGCCTGATAGTCAG
 10 CATATTGCGATCCTGGAATGAGCCTCTGTATCATCTGGTCACGGAAGTACGT
 GGTATGCAAGAAGCCCCGGAGGCTATCCTATCCAAAGCTGTAGAGATTGAGG
 AGCAAACCTAA (SEQ ID NO:26);

and

a concatamer of prolactin having the following amino acid sequence (the intervening sequences are underlined):

20 MLPICPGGAARCQVTLRDLDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITK
 AINSCHTSSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQE
 APEAILSKAVEIEEQTKKSMLPICPGGAARCQVTLRDLDRAVVLSHYIHNLS
 25 SEMFSEFDKRYTHGRGFITKAINSCHTSSLATPEDKEQAQQMNQKDFLSLIVSI
 LRSWNEPLYHLVTEVRGMQEAPPEAILSKAVEIEEQTK (SEQ ID NO:27),

30 which is encoded by the following DNA sequence (the intervening sequences are in bold):

ATGTTGCCCATCTGTCCCGCGGGGCTGCCCGATGCCAGGTGACCCCTTCGAG
 ACCTGTTTGACCGCGCCGTCGTCTGTCCCACTACATCCATAACCTCTCCTC
 35 AGAAATGTTTCAGCGAATTCGATAAACGGTATACCCATGGCCGGGGGTTTCATT
 ACCAAGGCCATCAACAGCTGCCACACTTCTTCCCTTGCCACCCCGAAGACA
 AGGAGCAAGCCCAACAGATGAATCAAAAAGACTTTCTGAGCCTGATAGTCAG
 40 CATATTGCGATCCTGGAATGAGCCTCTGTATCCTGGTCACGGAAGTACGT
 GGTATGCAAGAAGCCCCGGAGGCTATCCTATCCAAAGCTGTAGAGATTGAGG
 AGCAAACCGGTAAAGAATGTTGCCCATCTGTCCCGCGGGGCTGCCCGATGCC
 45 AGGTGACCCCTTCGAGACCTGTTTGACCGCGCCGTCGTCTGTCCCACTACATCC
 ATAACTCTCCTCAGAAATGTTTCAGCGAATTCGATAAACGGTATACCCATGGCC
 GGGGGTTTCATTACCAAGGCCATCAACAGCTGCCACACTTCTTCCCTTGCCACCC
 50 CCGAAGACAAGGAGCAAGCCCAACAGATGAATCAAAAAGACTTTCTGAGCCTGA
 TAGTCAGCATATTGCGATCCTGGAATGAGCCTCTGTATCATCTGGTCACGGAAG
 TACGTGGTATGCAAGAAGCCCCGGAGGCTATCCTATCCAAAGCTGTAGAGATTG
 55 AGGAGCAAACCTAA (SEQ ID NO:28)

Increase efficacy will occur with concatamers of the anti-angiogenic genes. This will increase the anti-angiogenic dosage level without changing the amount of vector necessary to deliver these genes. Similar to concatamers, a plasmid with two or more promoters, a plasmid with the IRES sequence (internal ribosomal entry site) between two sequences, and an antiangiogenic peptide with a secretory sequence will increase the delivery of genes to the therapeutic target without markedly increasing the DNA concentration. With regards to the concatamers, the concatamers can extend up to approximately 4400 bases in length (the coding region of a large protein), and the number of concatamers possible will depend on the number of bases of a single anti-angiogenic unit.

For fibronectin, the range of concatamers would be about 2 to 66. Although, the maximum number of anti-angiogenic units for the TSP1 is about 6, one can increase this concatameric number by deleting the sequences that do not have any anti-angiogenic effects, such as shown below:

ATG (CTGAGGCGGCCTCCCCTATGCTATCACAACGGAGTTCAGTACAGAAATAA
CGGTAAAAGATCCCCGTGGTCATCTTGTCTGTGACATGTGGTGATGGTGTGAT
GGTAAAAGAAGTGGTACCCTGTAGACAAGACAGTGGACACCTCCTCCCCAT)_nT
AA (SEQ ID NO:29),

where the corresponding amino acid sequence is:

M(LRRPPLCYHNGVQYRNNEEWTVDSGKSSPWSSCSVTCTCGDGVITRIGKSSPWD
ICSVTCGGGV)_n (SEQ ID NO:30),

and wherein n is an integer of from 2 to 24. In a similar manner, the concatameric number of the platelet factor-4 peptide, somatostatin inhibitor, angiostatin, and prolactin can be increased.

Since more than one anti-angiogenic pathway exists, concatamers consisting of two or more types of inhibitor are believed to be more effective than the homogenous concatamers. For example, heterogeneous concatamers of TSP1 and the fibronectin inhibitors can be inserted into the same vector. An example of a heterogeneous concatamer useful in present invention is as follows:

ATG (CTGAGGCGGCCTCCCCTATGCTATCACAACGGAGTTCAGTACAGAAATAA
CGGTAAAAGATCCCCGTGGTCATCTTGTCTGTGACATGTGGTGATGGTGTGAT
GGTAAAAGAAGTGGTACCCTGTAGACAAGACAGTGGACACCTCCTCCCCAT)_x(
TATATTGGTTCTCGTGGTAAAAGA)_yTAA (SEQ ID NO:31).

The first parenthetical represents the nucleotide sequence of TSP1, whereas the second parenthetical represents the anti-angiogenic fragment isolated from fibronectin, wherein x and y represent the number of repeats of TSP1 and fibronectin, respectively. Again, the number of bases delineated by the summation of x + y will generally not exceed 4400 bases.

The above heterogeneous concatamers need not be limited to only anti-angiogenic peptides. For example, the protein angiostatin or the large polypeptide fragment of prolactin can be modified with the above-mentioned genes which encode anti-angiogenic peptides. Again, the concatameric number will vary depending on the number of nucleotide bases of the unit angiogenic inhibitor. In this concatamer of large and small anti-angiogenic inhibitors, the ratio of large to small inhibitors is 0.1 to 0.9, preferably 1:1.

A translational start signal Met, has been included in all of the above peptides; and a transcriptional stop codon (TAA) has been included in all of the above DNA sequences.

The *Sa*I sites indicated in the above-sequences are a useful cloning tool for insertion of the DNA into BAP vector, which is known to be useful in expressing proteins efficiently *in vivo* from the β -actin promoter (Ray et al, *Genes Dev.*, 5:2265-2273 (1991)). Other restriction sites can be incorporated into the DNA for cloning into other vectors.

Other useful vectors for gene therapy which can be employed in the present invention include plasmids with a similar viral promoter, e.g., pZeoSV (Invitrogen); or the CMV promoter, e.g., pcDNA3, pRC/CMV or pcDNA1 (Invitrogen). Plasmids with a CMV promoter may contain an Intron 5' of the multiple cloning site (Zhu et al, *supra*). Plasmids contain-

ing the BGH terminator instead of the viral SV40 polyA terminator, e.g., pcDNA3, pRc/CMV, pRc/RSV (Norman et al, IBC's 5th Annual Meeting (1995); and Invitrogen vectors), can also be employed in the present invention so as to increase the expression of the tumor suppressor gene and the anti-angiogenic peptide in cells. As stated previously, a vector containing two or more promoters will greatly enhance the therapeutic efficacy. Vectors containing the IRES sequence which allows the translation of two different coding genes to occur from one mRNA transcript will also significantly increase the efficacy of the therapy.

Expression of the DNA encoding the tumor suppressor protein and the DNA encoding the anti-angiogenic peptide can be achieved using a variety of promoters, and the particular promoter employed is not critical to the present invention. For example, the promoter can be a generalized promoter, such as the β -actin promoter, a simian viral promoter, or the CMV promoter, or a tissue specific promoter, such as the α -fetal protein promoter which is specific for liver (Kaneko et al, *Cancer Res.*, 55:5283-5287 (1995), the tyrosinase promoter which is specific for melanoma cells (Hughes et al, *Cancer Res.*, 55:3339-3345 (1995); or the enolase promoter which is specific for neurons (Andersen et al, *Cell. Molec. Neurobiol.*, 13:503-515 (1993)).

The particular amount of DNA included in the cationic liposomes of the present invention is not critical. Generally, the amount of total DNA is in the range of about 0.005 to 0.32 $\mu\text{g}/\mu\text{M}$ of liposome, preferably 0.045 to 0.08 $\mu\text{g}/\mu\text{M}$ of liposome.

The DNA encoding a tumor suppressor gene is generally present in an amount of from 0.0025 to 0.16 $\mu\text{g}/\mu\text{M}$ of liposome, preferably 0.028 to 0.04 $\mu\text{g}/\mu\text{M}$ of liposome. The DNA encoding an anti-angiogenic peptide is generally present in an amount of from 0.0025 to 0.16 $\mu\text{g}/\mu\text{M}$ of liposome, preferably 0.028 to 0.04 $\mu\text{g}/\mu\text{M}$ of liposome.

The mole ratio of the DNA encoding the tumor suppressor gene to the DNA encoding the anti-angiogenic peptide is not critical to the present invention. Generally, the mole ratio is between 1:5 to 5:1, preferably about 1 to 1.

The DNA encoding the tumor suppressor gene and the anti-angiogenic peptide may be contained on the same vector, or on separate vectors.

Cationic liposomes are prepared similarly to other liposomes. In brief, the cationic lipid with/without DOPE are dissolved in a solvent, e.g., chloroform. The lipids are then dried in a round bottom flask overnight on a rotary evaporator. The resulting lipids are then hydrated with sterile water over a 1 hr period so form large multilamellar vesicle liposomes. To decrease the size of the liposomes, one may sonicate or pass the liposomes back and forth through a polycarbonate membrane. The DNA is then added to a solution containing the liposomes after their formation.

In another embodiment, the above-described objects of the present invention have been met by a method for inhibiting tumor growth in a subject comprising administering to a tumor-bearing subject a cationic liposome:DNA complex comprising DNA encoding a tumor suppressor gene and DNA encoding an anti-angiogenic peptide.

In a preferred embodiment the cationic liposome:DNA complex additionally comprises DNA encoding a tumor suppressor protein.

In a further preferred embodiment the cationic polymer :DNA complex additionally comprises DNA encoding a tumor suppressor protein. In a further preferred embodiment the cationic liposomes in the cationic liposome:DNA complex are comprised of one cationic lipid (i.e.- 1,2-dioleoyl-sn-glycero-3-ethyl-phosphocholine, 1,2-dimyristoyl-sn-glycero-3-ethylphosphocholine, and 2,3-diol-xyloxy)propyl-N,N,N'-tri-methyl-ammonium chloride) and may also be comprised of polyethylimine glycol (i.e., a pegylated lipid-1,2-diacy-sn-glycero-3-phospho-ethanolamine-N-Poly(ethylene glycol) 2000) and a targeted ligand (the amino acid peptide RGD, ferritin, or antibodies targeted toward to HER2).

In a further preferred embodiment of the invention said cationic liposomes in said complexes are comprised of one cationic polymer polyethylimine, polylysine, polyhistidine, and Superfect) and may also be comprised of polyethylene glycol and a targeted ligand (the amino acid peptide RGD, ferritin, or antibodies targeted toward to HER2, CEA).

In a further preferred embodiment said tumor suppressor protein in said complexes is selected from the group consisting of the p53, the p21 and the rb.

In a further preferred embodiment said tumor suppressor protein in the said complexes is p53.

In a further preferred embodiment of the invention said anti-angiogenic peptide in the said complexes is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, and SEQ ID NO:30.

In a further preferred embodiment the said DNA encoding an anti-angiogenic peptide used in the said cationic liposome:DNA complex is present in an amount of from 0.0025 to 0.16 $\mu\text{g}/\mu\text{M}$ of liposome.

In a further preferred embodiment the said DNA encoding an anti-angiogenic peptide in the said cationic polymer:DNA complex is present in an amount of from 0.016 to 0.33 $\mu\text{g}/\mu\text{g}$ of polymer.

In a further preferred embodiment the said DNA encoding a tumor suppressor protein in the said complexes is present in an amount of from 0.0025 to 0.16 $\mu\text{g}/\mu\text{M}$.

In a further preferred embodiment of the present invention said DNA encoding a tumor suppressor protein in the said complexes is present in an amount of from 0.016 to 0.33 $\mu\text{g}/\mu\text{M}$.

A further embodiment of the present invention is the provision of the use of a cationic polymer:DNA complex com-

prising DNA encoding an anti-angiogenic peptide for the production of a medicament for inhibiting tumor growth in a subject which preferably comprises administering the same to a tumor-bearing subject.

In a further preferred embodiment of the present invention the said complex in the said use additionally comprises DNA encoding a tumor suppressor protein.

5 In a further preferred embodiment of the present invention the said cationic liposome in the said use is (i.e. 1,2-dioleoyl-sn-glycero-3-ethylphosphocholine, 1,2-dimyristoyl-sn-glycero-3-ethylphosphocholine, and 2,3-dioleoyloxy)propyl-N,N,N-trimethylammonium chloride and may also be comprised of polyethylene glycol (i.e., a pegylated lipid-1,2-diacyl-sn-glycero-3-phosphoethanolamine-N-[Poly-(ethylene glycol) 2000] and a targeted ligand (the amino acid peptide RGD, ferritin, or antibodies targeted toward to HER2).

10 In a further preferred embodiment of the present invention the said cationic polymer in the said use is (i.e. poly-ethylimine Polycat57, polylysine, polyhistidine, and Superfect) and may also be comprised of polyethylene glycol and a targeted ligand (the amino acid peptide RGD, ferritin, or antibodies targeted toward to HER2).

In a further preferred embodiment of the present invention the said tumor suppressor protein used in the said cationic polymer is selected from the group consisting of p53, the p21 and the rb.

15 In a further preferred embodiment of the present invention the said tumor suppressor protein used in the said cationic polymer is p53.

In a further preferred embodiment the said anti-angiogenic peptide used for the said cationic polymer is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, and SEQ ID NO:30.

20 In a further preferred embodiment of the present invention the said DNA encoding an anti-angiogenic peptide used in the cationic complex is present in an amount from 0.0025 to 0.16 µg/pM of liposome or 0.016 to 0.33 µg/µg of polymer.

25 In a further preferred embodiment of the present invention the said DNA encoding a tumor suppressor protein used in the said complex is present in an amount of from 0.0025 to 0.16 µg/pM of liposome or 0.016 to 0.33 µg/µg of polymer.

In a further embodiment of the present invention the said cationic polymer:DNA complex comprising a plasmid with one or more promoters expressing either the same gene product (SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, and SEQ ID NO:30) or combinations of these gene products.

30 In a further embodiment of the present invention the cationic liposome:DNA complex comprising a plasmid with an intervening internal ribosomal entry site sequence between two genes (SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, and SEQ ID NO:29) that are either the same or different.

35 In a further preferred embodiment the said anti-angiogenic protein in the said cationic liposome:DNA complex or the said cationic polymer:DNA complex is secretory from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, and SEQ ID NO:30.

40 The particular type of tumor which can be treated in the present invention is not critical thereto. Examples of tumors which can be treated in accordance with the present invention include solid tumors, e.g., lung, colon, brain, breast and melanoma tumors. All of these tumors are very dependent on blood supply to sustain their growth.

The particular mode of administering the cationic liposome:DNA complex of the present invention is not critical thereto. Examples of such modes include intravenous, subcutaneous and intratumoral injections. Intravenous injection is the preferred administration mode since there is better distribution to the developing blood vessels of the tumor.

45 The amount of cationic liposome:DNA complex to be administered will vary depending upon the age, weight, sex of the subject, as well as the tumor volume and rate of tumor growth in the subject. Generally, the amount to be administered will be about 5 to 60 µg, preferably about 9 to 18 µg.

The following examples are provided for illustrative purposes only, and are in no way intended to limit the scope of the present invention.

60 EXAMPLE 1

Production of DNA Vectors

A. TSP1 Vector

55 The coding region of the TSP1 gene is well-known (GB Accession code-X14787). The TSP1 gene was inserted into the XbaI site of BAP vector (Ray et al. *supra*), so as to give rise to TSP1 vector, wherein expression of the TSP1 gene is controlled by the β-actin promoter.

More specifically, TSP1 cDNA and Bluescript plasmid (Promega) were digested with *Hind*I and *Xba*I, and then the TSP1 cDNA was ligated into Bluescript. Next, Bluescript containing the TSP1 cDNA and BAP vector were digested with *Sal*I and *Bam*HI, and TSP1 cDNA inserted in the *Xba*I site of BAP vector. The correct orientation of the TSP1 gene in BAP vector was confirmed by DNA sequencing.

B. TSP1 Vector

TSP1 vector is a vector containing a DNA fragment of the TSP1 gene which has the two anti-angiogenic domains (nucleotides 992-1650) (Tolsma et al, *supra*), and a start codon and a stop codon.

The DNA fragment was prepared by PCR using thrombospondin 1 cDNA as template, and 100 pmols of each of the following primers 5'-TAGGTCCTAGAATGACTGAAGAGAACAAAGAG-3' (SEQ ID NO:24); and 5'-ATGGTCTAGATT-AGAGACGACTACGTTTCTG-3' (SEQ ID NO:25) so as to amplify nucleotides 1013 to 1650 of the TSP1 gene. Both primers contain *Xba*I sites (underlined), the first primer contains an ATG start codon (in bold), and the second primer contains a TTA stop codon (in bold).

The resulting 638 base pair fragment of the TSP1 gene (hereinafter "TSP1") encodes the peptides that are known to be angiogenic inhibitors (Tolsma et al, *supra*).

After amplification, the DNA fragment was purified, digested with *Xba*I, and the digested fragment inserted into the *Xba*I site of BAP vector such that the expression of the TSP1 gene was controlled by the β -actin promoter (Ray et al, *supra*; and Lesoon-Wood et al, *Human Gene Ther.*, 8:395-405 (1995)). The correct orientation of the fragment in BAP vector was verified by digestion with *Bam*HI, and confirmed by DNA sequencing.

C. p53 Vector

The coding sequence of the p53 gene was cut from plasmid p1SVhp53c62 (Zakut-Houri et al, *EMBO J.*, 4:1261-1255 (1985)) with *Xba*I, and inserted into the multiple cloning sites of pGEM3Z vector (Promega, Madison, WI). Digestion of the resulting vector with *Sal*I and *Bam*HI generated a 1900 bp fragment that was then inserted into the *Sal*I and *Bam*HI sites of BAP vector such that expression of the p53 gene was controlled by the β -actin promoter. The correct orientation of the p53 gene in BAP vector was confirmed by DNA sequencing.

EXAMPLE 2

Preparation of Cationic Liposome:DNA Complexes

A DOTMA:DOPE liposome mixture is known to efficiently transfect endothelial cells *in vitro* (Tilkins et al, *Focus*, 16:117-119 (1994)). Accordingly, liposome:DNA complexes were prepared using DOTMA:DOPE, in a 1:1 ratio, essentially as described by Debs et al, *J. Biol. Chem.*, 265:10189-10192 (1990). Similar liposomes preparations can be prepared by mixing, at a 1:1 ratio, DOPE with other cationic lipids, such as, 1,2-dioleoyl-sn-glycero-3-ethylphosphocholine, and 1,2-dimyristoyl-sn-glycero-3-ethylphosphocholine.

More specifically, a mixture of 400 nmoles of the DOTMA and DOPE were dried overnight on a rotary evaporator. Then, the lipids were rehydrated with 1.5 ml of water for 2 hrs. Next, the milky liposome preparation was sonicated with a bath sonicator until clear. The resulting liposome preparation was then passed through a 50 nm polycarbonate filter between 15 to 20 times with a LipsoFast-Basic extruder (Avestin, Ottawa, On).

The DNA employed was either (1) empty BAP vector; (2) TSP1 vector alone; (3) TSP1 vector alone; (4) p53 vector alone; (5) p53 vector + TSP1 vector; or (6) p53 vector + TSP1 vector.

The DNA was prepared with the max Qiagen kits (Qiagen Inc., Chatsworth, Ca), and washed twice in 70% (v/v) ethanol. The DNA was then dialyzed against water for 24 hrs to removed any remaining salt.

About 400 pmols of the liposome preparation was gently mixed with between 18 to 35 μ g of total DNA in an Eppendorf tube. This amount in each eppendorf tube was sufficient for two injections. The same amount of DNA was injected in the combination therapies as in the single treatment regimens. For example, if 16 μ g of DNA in the combination therapy (8.0 μ g of p53 + 8.0 μ g of TSP1) was injected into each mouse of one group, then 16 μ g of p53 was injected into each mouse of a second group.

EXAMPLE 3

Anti-Angiogenic Effect of Cationic Liposome:DNA Complexes

The anti-angiogenic effects of the cationic liposome:DNA complexes obtained in Example 2 were evaluated in mice containing MDA-MB-435 breast cancer tumors (American Type Tissue Culture, Bethesda, MD), which are p53 defi-

cient.

More specifically, after administering the anesthetic, Metofane, to 126 female athymic nude mice (NCI), the mice were injected with 2.0×10^5 MDA-MB-435 tumor cells into the mammary fat pad using a stepper (Tridax) and a 27.5 g needle. Two weeks later, the mice whose tumors grew were divided into various treatment regimens, 18 mice per each regimen. The treatment regimens were as follows:

(1) untreated; (2) empty BAP vector; (3) TSP1 vector alone; (4) TSP1 vector alone; (5) p53 vector alone; (6) p53 vector + TSP1 vector; and (7) p53 vector + TSP1 vector. The mice received two intravenous injections, the first injection 14 days after the malignant cells had been implanted into the mice, and the second injection 24 days after the malignant cells had been implanted into the mice. The first injection consisted of 200 pmols of the liposomes complexed with 16 μ g of total DNA. The second injection consisted of 200 pmols of the liposomes complexed with 8.0 μ g of total DNA. The sizes of the tumors were measured 7 days after the second injection. The results are shown in Table 1 below.

TABLE 1

Anti-tumor Effects of TSP1 and TSP1	
Putative Anti-tumor Genes	Tumor Size (mm ³)
Untreated	113.5 \pm 6.41
BAP	102.8 \pm 8.83
TSP1	103.2 \pm 8.96
TSP1	89.4 \pm 11.06
p53	80.1 \pm 12.7*
p53 + TSP1	82.9 \pm 6.95*
p53 + TSP1	53.2 \pm 8.37**

* p53 or p53 + TSP1 vs. untreated, $p < 0.05$

** p53 + TSP1 vs. untreated or BAP, $p < 0.01$

As shown in Table 1 above, the p53-treated group was found to be statistically different from the untreated group ($p < 0.05$) after 2 injections. However, the p53 treated group was not statistically different from the empty BAP vector group. This was similar to the results described by Lesoon-Wood et al, *Human Gene Ther.*, 6:395-406 (1995), in which p53 was not statistically different from the empty BAP vector group until after 5 injections.

However, p53 in combination with TSP1 reduced tumors more effectively than p53 alone. That is, after just 2 injections of this combination therapy, there was a 35% further reduction in tumor growth compared to p53 alone. The combination group was statistically different from both the untreated and the empty BAP vector groups ($p < 0.01$). Although TSP1 by itself was slightly less effective than p53, TSP1 was, unexpectedly, substantially more effective than TSP1. In fact, the full length TSP1-treatment group had no more effect than either the empty vector or the untreated groups. This was unexpected for several reasons: 1) both the full length and the fragment of thrombospondin 1 contained the anti-angiogenic peptide 2) in a previous ex vivo study (Weinstat-Saslow et al, supra), full length thrombospondin 1 was effective in inhibiting tumor growth, and 3) full length thrombospondin 1 has a secretory sequence presumably so that the secreted protein can inhibit endothelial proliferation, whereas the thrombospondin 1 fragment does not contain a secretory sequence.

Regardless of whether there is a secretory sequence, one would predict prior to the present invention that the liposome:antiangiogenic gene would not be an effective antitumor therapy. As taught by Lesoon-Wood et al., the transfection efficiency of the tumor with cationic liposomes was very low. In fact, it could not be quantitated with a primer extension method. We know from the teaching of Weinstat-Saslow et al. that high levels of expressed TSP1 in 100% of the tumor cells reduces the tumor growth by only 60% in an ex vivo system. Extrapolating from these findings, a relatively high transfection efficiency of 20% with the liposome: antiangiogenic genes would have resulted in a marginal reduction ($20\%/100\% \times 60\% \text{ reduction} = 12\%$) of the tumor. This amount of tumor reduction would not have resulted in statistical differences with the liposome:antiangiogenic gene complexes. A transfection efficiency of the tumor above 10% would have easily been measurable with a variety of techniques including the primer extension method (used by Lesoon-Wood et al.). It has been determined that the transfection efficiency of the tumor is less than 5% with these cationic liposomes.

Hence, it was clearly unobvious that DNA encoding an anti-angiogenic peptide alone would be an effective anti-

tumor agent *in vivo*, based upon teachings that an anti-angiogenic peptide is an effective anti-tumor agent (Tolsma et al and Bouck et al), and based upon the teachings that DNA encoding a full-length anti-angiogenic protein is an effective anti-tumor agent *ex vivo* (Weinstat-Sastow et al).

A second experiment was carried out to determine whether the combination therapy of p53 and TSP1 was effective at lower dosages, and to confirm that the combination of p53 and TSP1 reduced the tumor size considerably more than p53 alone.

More specifically, 36 mice were injected with 2.0×10^5 MDA-MB-435 tumor cells into the mammary fat pad. Two weeks later, the mice whose tumors grew were divided into various treatment regimens, 18 mice per each regimen. The treatment regimens were as follows: (1) empty BAP vector; (2) p53 vector alone, and (3) p53 vector + TSP1 vector. The mice were injected intravenously with 200 pmols of the liposomes complexed with 8.0 μ g of total DNA. Subsequently, the mice were treated in the same manner with 200 pmols of the liposomes complexed with 12 μ g of total DNA for the next 4 injections. Ten days elapsed between each injection. The sizes of the tumors were measured before each injection and 7 days after the last injection. The results are shown in Table 2 below:

TABLE 2

Anti-tumor Effects of p53 and TSP1	
Putative Anti-tumor Genes	Tumor Size (mm ³)
BAP	855±345
p53	616±142
p53 + TSP1	265±133*

* p53 + TSP1 vs. BAP, $p < 0.02$

As shown in Table 2 above, the combination therapy with p53 and TSP1 was statistically different from BAP, whereas the p53 alone treatment was not. This experiment confirmed that p53 and TSP1 were more effective than p53 alone. Furthermore, a different dosage regimen, without an initial booster dose of 16 μ g of DNA as used in the experiment in Table 1, accentuated the difference between the combination treatment and the p53 alone treatments.

In table 1, the TSP1 treatment group decreased the tumor more than empty vector or untreated groups. However, it was not statistically significant ($p = .07$). We repeated the experiment after injecting a higher dose of DNA and measured the different treatment groups tumors 10 days after the first treatment.

Table 3

Anti-tumor Effects of TSP1	
Putative Anti-tumor Genes	Tumor Size (mm ³)
Untreated	80.0±11.2
BAP	80.4±4.5
TSP1	50.7±4.6*

* TSP1 vs. BAP, $p < 0.025$

At the higher dose of 19 μ g of DNA, the TSP1 treatment group was statistically different from either the empty vector or the untreated groups.

In another experiment demonstrating the efficacy of antiangiogenic genes, various antiangiogenic genes were examined for their antitumor activity. After administering the anesthetic, Metofane, to 126 female athymic nude mice (NCI), the mice were injected with 3.0×10^5 MDA-MB-435 tumor cells into the mammary fat pad using a syringe (Tridax) and a 27.5 g needle. Two weeks later, the mice whose tumors grew were divided into various treatment regimens, 8 mice per each regimen. The treatment regimens were as follows: (1) BAP vector; (2) TSP1 vector alone; (3) laminin peptide vector alone; and (4) angiostatin vector alone. The mice received 4 intravenous injections, the first injection was 10 days after the malignant cells had been implanted into the mice, and the remaining injections were thereafter 10 days apart. The injections consisted of 200 pmols of the liposomes complexed with 12.5 μ g of total DNA. The results are

shown in Table 4 below.

TABLE 4

Putative Anti-tumor Genes	Tumor Size(mm ³)
BAP	194.7 ± 11.8
TSP1	135.9 ± 11.9*
Laminin peptide	126.4 ± 8.4*
Angiostatin	95.2 ± 6.3* ^{**}

* TSP1, Laminin peptide, and Angiostatin vs. BAP, p<0.05

^{**} Angiostatin vs. BAP, p<0.01

As shown in Table 4 above, the cationic liposomes containing only DNA encoding various anti-angiogenic peptides (TSP1, laminin peptide and angiostatin) significantly inhibited tumor growth.

Next, MCF7 cells (American Type Tissue Culture, Bethesda, MD), which are a breast cancer cell line with two normal p53 alleles, were evaluated as described above except that 4.0×10^6 cells were injected into the mice; and the third injection contained 12 µg of the DNA. Each injection was 10 days apart. Nine mice were injected with each of the following treatments except for regimen (1), in which 8 mice were treated: (1) untreated; (2) BAP; (3) p53; and (4) p53 + TSP1. The sizes of the tumors were measured 7 days after the third injection. The results are shown in Table 5 below.

TABLE 5

Effect of p53 and TSP1 on MCF7s Cells	
Putative Anti-tumor Genes	Tumor Size (mm ³)
Untreated	124.6 ± 7.3
BAP	136 ± 16.8
p53	83.1 ± 13.6*
p53 + TSP1	69.0 ± 13 ^{**}

* p53 vs. untreated or BAP, p<0.05

^{**} p53 + TSP1 vs. untreated or BAP, p<0.01

As shown in Table 5 above, the most effective therapy against MCF7s was p53 and TSP1. The significance level for the p53 + TSP1 therapy was greater than for p53 alone when they were compared against either the untreated or the BAP groups.

The above experiment verifies that p53 and TSP1 decreased the MCF7s tumor more than the p53 treated or the untreated groups. 4×10^5 MCF7 cells were injected bilaterally into the mammary fat pads of the 28 nude mice. After two weeks of growth, these mice were randomly divided into four groups: 1) empty vector, 2) p53, 3) p53 + TSP1, and 4) untreated. The mice received one injection of 200 pmoles of liposomes complexed with 14 µg of DNA, and the tumors from the various treatment groups were measured 10 days after the treatment. The results are shown in Table 6 below.

Table 6

Putative Anti-tumor Genes	Tumor Size (mm ³)
Empty vector-	54.7±4.0
p53	45.5±5.0
p53 + TSP1	33.9±3.6*
Untreated	61.9±8.3

* p53 + TSP1 vs Untreated, $p < 0.025$

As shown in Table 6, the additional reduction of the tumor by the combined use of p53 and TSP1 (also in Tables 1, 2, and 4 above) compared to the use of p53 only, suggest that TSP1 and p53 have different mechanisms of action. Although this does not preclude that the target of p53 is the vasculature of the tumor, the mechanism of inhibition of the tumor by p53 is not known at present. However, any mechanism of tumor inhibition by p53 and/or thrombospondin 1 must account for the low transfection efficiency of the tumor. Again, with a liposome complexed to a chloramphenicol acetyltransferase marker, it has been demonstrated that less than 5% of the tumor derived from MDA-MB-435 cells was transfected with the marker gene.

Besides p53 and the antiangiogenic fragment of thrombospondin 1, we determined that liposomes complexed to DNA encoding the laminin peptide inhibits tumor growth. More specifically, after administering the anesthetic, Metofane, to 24 female athymic nude mice, the mice were injected with 3.0×10^5 MDA-MB-435 tumor cells into the mammary fat pad using a stepper and a 27.5 g needle. Two weeks later, the mice whose tumors grew were divided into various treatment regimens, 8 mice per each regimen. The treatment regimens were as follows: (1) BAP, (2) laminin, and (3) p53 + laminin. The mice were injected intravenously with 200 pmols of the liposomes complexed with 12.5 mgs of total DNA 6.25 mg of each vector when a combination was used. The mice then received 3 injections, each 10 days apart. The tumors were measured at the time of each injection and at the time of the last injection. The results are shown in Table 7 below.

TABLE 7

Putative Anti-tumor genes	Tumor Size (mm ³)
BAP	345 ± 23.5
Laminin peptide	280 ± 32.4
Laminin peptide + p53	192 ± 10.5*

* BAP vs. Laminin peptide + p53, $p < 0.05$

As shown in Table 7 above, cationic liposomes containing a combination of DNAs encoding laminin peptide + p53 was unexpectedly more effective in reducing tumor growth than when DNA encoding the anti-angiogenic peptide was used alone. Thus, the addition of a tumor suppressor gene, p53, enhances the anti-tumor effect of the anti-angiogenic peptide.

Although intravenous injection are preferred, the method of administration of the liposome:DNA complex is not critical. In figure 1, it was found that intratumoral injections are effective, and it also supports that the therapy is effective against tumors other than breast cancer. In this experiment, 18 mice were injected with 3×10^5 C6 glioma cells (rat brain tumors) subcutaneously. Six days after the injections of these cells, the mice were separated into 3 groups: 1) BAP, 2) FLK-DN (a dominant negative receptor), and 3) angiostatin. After the second intratumoral injection, there was a statistical difference between the angiostatin and the BAP groups. Thus, this therapy is effective when given intratumorally and is effective as expected tumors other than breast tumors.

It was also found that this liposome: secretory angiostatin construct was more effective than the non-secreted analog. In brief, we injected 24 nude mice with 3×10^5 MDA-MB-435 cells inserted at the 5 prime end of the their construct. Two weeks later the mice were divided into three groups, they received the following therapies intravenously: 1) liposome: BAP, 2) liposome: secreted angiostatin, and 3) liposome: angiostatin. The concentration of DNA injected into the

mice was 14.5 ugs. The mice received one injection of the liposome:DNA complex and their tumors were measured 10 days after the injection.

Table 8

Efficacy of Secretory Angiostatin	
Therapeutic Genes	Tumor Size (mm ³)
Angiostatin	28.8±2.2
Angiostatin-Secretory	18.6±1.8*
BAP	30.5±3.3

* $p < 0.05$, BAP vs. Angiostatin-secretory

As seen in table 8, the secretory angiostatin treatment group was much more effective than the empty vector control or the angiostatin treatment group in reducing the size of the tumor. From this experiment, it is evident that a secretory sequence inserted into the 5' portion of the antiangiogenic inhibitor will increase its efficacy.

In vitro assays indicate that cationic polymers will significantly improve the present therapy. When a carrier such as a cationic lipid was used in this *in vitro* assay, the inhibitory effect (of the genes p53, TSP1, and the combination of p53 and TSP1) was marginal whereas another vector, Superfect (a cationic polymer), was much more effective as a carrier. This is because Superfect was 15 times more effective than the cationic liposomes in transfecting endothelial cells with the CAT marker. The cationic liposomes used in this section was DOSPER (Boehringer), which of the 14 lipids tested gave the best results. Included in this panel of 14 lipids that we tested was lipofectin (BRL) which is a mixture of DOTMA/DOPE that we have used in an *in vivo* study. In brief, we plated 1×10^5 Huvec cells into each well of a 6 well plate. 25 uL of Superfect complexed with 2 ugs of DNA was added to each plate 24 hours after the initial seeding of the cells. 36 hours after the transfection, the cells were lysed and the amount of CAT protein was assayed.

Table 9

Vectors	Activity(DPMs/protein)
Cationic liposomes with BAP	31.1±7.2
Cationic liposomes with CAT	682±129
Superfect with BAP	21.4±0.458
Superfect with CAT	10816±687*
$p < 0.001$, Superfect-CAT vs Cationic liposome-CAT	

This experiment clearly demonstrates that this cationic polymer is a superior in the transfection of endothelial cells, which is a likely target of the therapeutic gene. We have found that Superfect is a better transfection agent than cationic liposomes for many different cell lines. Since Superfect which is a cationic polymers is such an efficient carrier of DNA, this underscores possibility that non-viral carriers as a class of carriers will be effective in decreasing the tumor size. As a result, other non-viral carriers besides liposomes should be included in this patent.

Transfection of Huvec Cells with various inhibitors was as follows. 1.0×10^5 Huvec cells (Clonetics), a human endothelial cell line, were plated into each well of a 6-well plate, and placed in a CO₂ incubator at 37°C. Twenty-four hours later, the cells were transfected with 25 uL of Superfect (Qiagen), a cationic polymer, complexed to 2.0 mg of various DNA vectors, i.e., (1) BAP vector; (2) p53 vector; (3) TSP1 vector; and (4) p53 vector + TSP1 vector. After the cells were exposed for 2 hours to this complex at 37°C, the media was removed, and replaced with fresh EGM media (Clonetics, Inc.) containing 10% (v/v) fetal calf serum, and 1.0% (w/v) glutamine, and the cells placed in a CO₂ incubator at 37°C. Twenty-four hours later, the cell number in each plate was determined by the 3-(4,5-dimethylthiazol-2-yl)-(3-carboxymethoxyphenyl)-2,5-di-phenyltetrazolium bromide (MTS) assay described by Butke et al, *J. Immunol. Methods*, 157:233-240 (1993).

The results are shown in Figure 1 attached hereto dealing with the intratumoral injections of liposome:DNA complexes and its effect on the tumor dimension 6 to 12 days after injection.

As shown in Figure 1, it was found that p53, TSP1, and the combination therapy of p53 and TSP1 were effective at inhibiting endothelial cells *in vitro*. The combination of p53 and TSP1 was the most effective at inhibiting endothelial

cells. There was a close correlation between the therapeutic genes reducing the tumor size *in vivo* and their effects on endothelial cell number *in vitro*.

Figure 2 shows the effect of different treatment groups on endothelial cells *in vitro*. it was found that the percentage of BAP control is significantly decreased when using BAP-p53 and BAP1-TSP1 as treatment groups. A further synergistic decrease is achieved when using BAP-p53/TSP1 as the treatment group.

While the invention has been described in detail, and with reference to specific embodiments thereof, it will be apparent to one of ordinary skill in the art that various changes and modifications can be made therein without departing from the spirit and scope thereof.

10

15

20

25

30

35

40

45

50

55

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Archibald James MIXSON
 (B) STREET: 1 Baedarwood Ct.
 10 (C) CITY: Rockville
 (D) STATE: Maryland
 (E) COUNTRY: USA
 (F) POSTAL CODE (ZIP): 21201

15 (ii) TITLE OF INVENTION: CATIONIC VEHICLE:DNA COMPLEXES AND THEIR
 USE IN GENE THERAPY

(iii) NUMBER OF SEQUENCES: 33

20 (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

25 (v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: EP 97112154.6

(2) INFORMATION FOR SEQ ID NO: 1:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

40 Met Thr Glu Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu
 1 5 10 15
 Cys Tyr His Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val
 20 25 30
 45 Asp Ser Cys Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys
 35 40 45
 Lys Val Ser Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp
 50 55 60
 55 Glu Glu Cys Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly
 65 70 75 80

EP 0 819 758 A2

Trp Ser Pro Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn
85 90 95

5 Gly Ile Gln Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys
100 105 110

Glu Gly Ser Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp
115 120 125

10 Lys Arg Phe Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser
130 135 140

Ser Cys Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Thr Leu Cys
145 150 155 160

15 Asn Ser Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala
165 170 175

Arg Glu Thr Lys Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Glu
180 185 190

20 Gly Trp Gly Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly
195 200 205

25 Gly Gly Val Gln Lys Arg Ser Arg Leu
210 215

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

40 ATGACTGAAG AGAACAAAGA GTTGGCCAAT GAGCTGAGGC GGCCTCCCCT ATGCTATCAC 60
AACGGAGTTC AGTACAGAAA TAACGAGGAA TGGACTGTGT ATAGCTGCAC TGAGTGTAC 120
45 TGTCAAGACT CAGTTACCAT CTGCAAAAAG GTGTCTGCCC CCATCATGCC CTGCTCCAAT 180
GCCACAGTTC CTGATGGAGA ATGCTGTCTT CGCTGTGGGC CCAGCGACTC TCGGACGAT 240
GGCTGTCTCT CATGGTCCGA GTGGACCTCC TGTCTACGA GCTGTGGCAA TGGAAATCAG 300
50 CAGCGCGGCC GCTCCTGCGA TAGCCTCAAC AACCGATGTG AGGGCTCCTC GGTCCAGACA 360
CGGACCTGCC ACATTCAGGA GTGTGACAAA AGATTAAAC AGGATGGTGG CTGGAGCCAC 420

EP 0 819 758 A2

TGGTCCCCGT GGTCACTCTG TTCTGTGACA TGTTGGTGATG GTGTGATCAC AAGGATCCGG 480
 CTCTGCAACT CTOCCAGCCC CCAGATGAAT GGGAAACCCCT GTGAAGGCGA AGCGCGGGAG 540
 ACCAAGCCT GCAAGAAAGA CGCTGCCCC ATCAATGGAG GCTGGGGTCC TTGGTCACCA 600
 TGGGACATCT GTTCTGTAC CTGTGGAGGA GGGGTACAGA AACGTAGTCT CTCTAA 656

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met	Thr	Glu	Asn	Lys	Glu	Leu	Ala	Asn	Glu	Leu	Arg	Arg	Pro	Pro	Leu	1	5	10	15
Cys	Tyr	His	Asn	Gly	Val	Gln	Tyr	Arg	Asn	Asn	Glu	Glu	Trp	Thr	Val	20	25	30	
Asp	Ser	Cys	Thr	Glu	Cys	His	Cys	Gln	Asn	Ser	Val	Thr	Ile	Cys	Lys	35	40	45	
Lys	Val	Ser	Cys	Pro	Ile	Met	Pro	Cys	Ser	Asn	Ala	Thr	Val	Pro	Asp	50	55	60	
Glu	Glu	Cys	Cys	Pro	Arg	Cys	Trp	Pro	Ser	Asp	Ser	Ala	Asp	Asp	Gly	65	70	75	80
Trp	Ser	Pro	Trp	Ser	Glu	Trp	Thr	Ser	Cys	Ser	Thr	Ser	Cys	Gly	Asn	85	90	95	
Gly	Ile	Gln	Gln	Arg	Gly	Arg	Ser	Cys	Asp	Ser	Leu	Asn	Asn	Arg	Cys	100	105	110	
Glu	Gly	Ser	Ser	Val	Gln	Thr	Arg	Thr	Cys	His	Ile	Gln	Glu	Cys	Asp	115	120	125	
Lys	Arg	Phe	Lys	Gln	Asp	Gly	Gly	Trp	Ser	His	Trp	Ser	Pro	Trp	Ser	130	135	140	
Ser	Cys	Val	Thr	Cys	Gly	Asp	Gly	Val	Ile	Thr	Arg	Ile	Thr	Leu	Cys	145	150	155	160
Asn	Ser	Pro	Ser	Pro	Gln	Met	Asn	Gly	Lys	Pro	Cys	Glu	Gly	Glu	Ala	165	170	175	
Arg	Glu	Thr	Lys	Lys	Ala	Cys	Lys	Lys	Asp	Ala	Cys	Pro	Ile	Asn	Glu	180	185	190	

EP 0 819 758 A2

5 Gly Trp Gly Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly
195 200 205

6 Gly Gly Val Gln Lys Arg Ser Arg Leu Cys Val His Ser Arg Met Thr
210 215 220

10 Glu Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr
225 230 235 240

His Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser
245 250 255

15 Cys Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val
260 265 270

Ser Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Glu Glu
275 280 285

20 Cys Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser
290 295 300

Pro Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile
305 310 315 320

25 Gln Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly
325 330 335

Ser Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg
340 345 350

30 Phe Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys
355 360 365

Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Thr Leu Cys Asn Ser
370 375 380

35 Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu
385 390 395 400

Thr Lys Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Glu Gly Trp
405 410 415

40 Gly Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly
420 425 430

45 Val Gln Lys Arg Ser Arg Leu
435

(2) INFORMATION FOR SEQ ID NO: 4:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

5
 10
 15
 20
 25
 30
 35
 40
 45
 50
 55

ATGACTGAAG AGAACAAAGA GTTGGCCAAT GAGCTGAGGC GGCCTCCCCCT ATGCTATCAC 60
 AACCGAGTTC AGTACAGAAA TAACGAGGAA TGGACTGTTG ATAGCTGCAC TGAGTGTAC 120
 TGTCAGAACT CAGTTACCAT CTGCAAAAAG GTGTCTTGCC CCATCATGOC CTGCTCCAAT 180
 GCCACAGTTC CTGATGGAGA ATGCTGTCTT CGCTGTGTGG CCAGCGACTC TGGCGACGAT 240
 GGCTGGTCTC CATGGTCCGA GTGGACCTCC TGTTCTACGA GCTGTGGCAA TGGAAATTCAG 300
 CAGCGCGGCC GCTCTGCGA TAGCCTCAAC AACCGATGTG AGGGCTCCTC GGTCCAGACA 360
 CGGACCTGCC ACATTACGGA GTGTGACAAA AGATTAAAC AGGATGGTGG CTGGAGCCAC 420
 TGGTCCCCGT GGTCTCTTGG TTCTGTGACA TGTGGTGATG GTGTGATCAC AAGGATCCCG 480
 CTCTGCAACT CTCCAGCCCC CCAGATGAAT GGGAAACCCT GTGAAGGCGA AGCGCGGGAG 540
 ACCAAGCCT GCAAGAAAGA CGCTGCCCC ATCAATGGAG GCTGGGGTCC TTGGTCACCA 600
 TGGGACATCT GTTCTGTAC CTGTGGAGGA GGGGTACAGA AACGTAGTCG TCTCTGCGTC 660
 GACTCTAGAA TGAATGAAGA GAACAAAGAG TTGGCCAATG AGCTGAGCGG GCCTCCCCCTA 720
 TGCTATCACA ACGGAGTTCA GTACAGAAAT AACGAGGAAT GGACTGTTGA TAGCTGCACT 780
 GAGTGTCACT GTCAGAACTC AGTTACCATC TGCAAAAAGG TGTCTGCCCC CATCATGCCC 840
 TGCTCCAATG CCACAGTTCG TGATGGAGAA TGCTGTCTCT GCTGTGGGCC CAGCGACTCT 900
 GCGGACGATG GCTGGTCTCC ATGGTCCGAG TGGACCTCCT GTTCTACGAG CTGTGGCAAT 960
 GGAATTCAGC AGCGCGGCCG CTCCTGCGAT AGCCTCAACA ACCGATGTGA GGGCTCCTCG 1020
 GTCCAGACAC GGACCTGCCA CATTACAGGAG TGTGACAAA GATTAAACA GGATGGTGGC 1080
 TGGAGCCACT GGTCCCCGTG GTCATCTTGT TCTGTGACAT GTGGTGATGG TGTGATCACA 1140
 AGGATCCGGC TCTGCAACTC TCCAGCCCC CAGATGAATG GGAAACCCTG TGAAGGCGAA 1200
 GCGCGGGAGA CCAAGCCTG CAAGAAGAC GCCTGCCCCA TCAATGGAGG CTGGGGTCTT 1260
 TGGTACCAT GGGACATCTG TTCTGTCAAC TGTGGAGGAG GGTACAGAA ACGTAGTCGT 1320
 CTCTAA 1326

(2) INFORMATION FOR SEQ ID NO: 5:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Tyr Ile Gly Ser Arg
 1 5

(2) INFORMATION FOR SEQ ID NO: 6:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GTCGACATGT ATATTGGTTC TCOTTAAGTC GAC

33

(2) INFORMATION FOR SEQ ID NO: 7:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Tyr Ile Gly Ser Arg Gly Lys Ser Tyr Ile Gly Ser Arg Gly Lys
 1 5 10 15
 Ser Tyr Ile Gly Ser Arg Gly Lys Ser
 20 25

(2) INFORMATION FOR SEQ ID NO: 8:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GTCGACATGT ATATTGGTTC TCGTGTA AAA GATATATGG TTCTCGTGGT AAAAGATATA 60

TTGGTTCTCG TGGTAAAAGA TAAGTCGACC 90

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Met Leu Tyr Lys Lys Ile Ile Lys Lys Leu Leu Glu Ser
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GTCGACATGC TTTATAAGAA GATCATCAAG AAGCTTCTTG AGAGTTAAGT CGAC 54

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

EP 0 819 758 A2

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Met Leu Tyr Lys Lys Ile Ile Lys Lys Leu Leu Glu Ser Gly Lys Ser
 1 5 10 15
 Leu Tyr Lys Lys Ile Ile Lys Lys Leu Leu Glu Ser Gly Lys Ser Leu
 20 25 30
 Tyr Lys Lys Ile Ile Lys Lys Leu Leu Glu Ser Gly Lys Ser
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GTCGACATGC TTTATAAGAA GATCATCAAG AAGCTTCTTG AGAGTGGTAA AAGACTTTAT 60
 AAGAAGATCA TCAAGAAGCT TCTTGAGAGT GGTAAAGAC TTTATAAGAA GATCATCAAG 120
 AAGCTTCTTG AGAGTGGTAA AAGATAAGTC GAC 153

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Met Phe Cys Tyr Trp Lys Val Cys Trp
 1 5

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GTCGACATGT TCTTGATTG GAAGGGATTG TGGTAAGTCG AC 42

(2) INFORMATION FOR SEQ ID NO: 15:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

25 Met Phe Cys Tyr Trp Lys Val Cys Trp Gly Lys Ser Phe Cys Tyr Trp
1 5 10 15

Lys Val Cys Trp Gly Lys Ser Phe Cys Trp Lys Val Cys Trp Gly Lys
20 25 30

30 Ser

(2) INFORMATION FOR SEQ ID NO: 16:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GTCGACATGT TCTTGATTG GAAGGGATTG TGGGTAAAA GATTCTTGTA TTGGAAGGGA 60

TTGTGGGGTA AAAGATTCTT GTATTGGAAG GGATTGTGGG GTAAAAGATA AGTCGAC 117

50 (2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

55

5 (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Met Gly Arg Gly Asp
1 5

15 (2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GTGACATGT CTTGTCTTG GAAGACTTG ACTTAAGTCG AC

42

30 (2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Met Gly Arg Gly Asp Gly Lys Ser Gly Arg Gly Asp Gly Lys Ser Gly
1 5 10 15

45 Arg Gly Asp Gly Lys Ser
20

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
50 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GTGACATGG GTCGTGGTGA TGGTAAAAGA GTCGTGGTG ATGGTAAAAG AGGTCGTGGT 60
GATGGTAAAA GATAAGTCGA C 81

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Met Val Tyr Leu Ser Glu Cys Lys Thr Gly Ile Gly Asn Gly Tyr Arg
1 5 10 15
Gly Thr Met Ser Arg Thr Lys Ser Gly Val Ala Cys Gln Lys Trp Gly
20 25 30
Ala Thr Phe Pro His Val Pro Asn Tyr Ser Pro Ser Thr His Pro Asn
35 40 45
Glu Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Glu Gln
50 55 60
Gly Pro Trp Cys Tyr Thr Thr Asp Pro Asp Lys Arg Tyr Asp Tyr Cys
65 70 75 80
Asn Ile Pro Glu Cys Glu Glu Glu Cys Met Tyr Cys Ser Gly Glu Lys
85 90 95
Tyr Glu Gly Lys Ile Ser Lys Thr Met Ser Gly Lys Asp Cys Gln Ala
100 105 110
Trp Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ala Lys Phe
115 120 125
Pro Ser Lys Asn Leu Lys Met Asn Tyr Cys His Asn Pro Asp Gly Glu
130 135 140
Pro Arg Pro Trp Cys Phe Thr Thr Asp Pro Thr Lys Arg Trp Glu Tyr
145 150 155 160

EP 0 819 758 A2

Cys Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Pro Ser Pro Thr
 165 170 175
 Tyr Gln Cys Leu Lys Gly Arg Gly Glu Asn Tyr Arg Gly Thr Val Ser
 180 185 190
 Val Thr Val Ser Gly Lys Thr Cys Gln Arg Trp Ser Glu Gln Thr Pro
 195 200 205
 His Arg His Asn Arg Thr Pro Glu Asn Phe Pro Cys Arg Asn Leu Glu
 210 215 220
 Glu Asn Tyr Cys Arg Asn Pro Asp Gly Glu Thr Ala Pro Trp Cys Tyr
 225 230 235 240
 Thr Thr Asp Ser Gln Leu Arg Trp Glu Tyr Cys Glu Ile Pro Ser Cys
 245 250 255
 Glu Ser Ser Ala Ser Pro Asp Gln Ser Asp Ser Ser Val Pro Pro Glu
 260 265 270
 Glu Gln Thr Pro Val Val Gln Glu Cys Tyr Gln Ser Asp Gly Gln Ser
 275 280 285
 Tyr Arg Gly Thr Ser Ser Thr Thr Ile Thr Gly Lys Lys Cys Gln Ser
 290 295 300
 Glu Gln Thr Pro His Arg
 305 310

(2) INFORMATION FOR SEQ ID NO: 22:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 645 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GTCGACATGG TGTATCTGTC AGAATGTAAAG ACCGGCATCG GCAACGGCTA CAGAGGAACC 60
 ATGTCCAGGA CAAAGAGTGG TGTTGCCTGT CAAAAGTGGG GTGCCACGTT CCCCCACGTA 120
 CCCAACTACT CTCCCACTAC ACATCCCAAT GAGGGACTAG AAGAGAACTA CTGTAGGAAC 180
 CCAGACAATG ATGAACAAGG GCCTTGGTGC TACACTACAG ATCCGGACAA GAGATATGAC 240
 TACTGCAACA TTCTTGAATG TGAAGAGGAA TGCATGTACT GCAGTGGAGA AAAGTATGAG 300
 GGCAAAATCT CCAAGACCAT GTCTGGACTT GACTGCCAGG CCTGGGATTC TCAGAGCCCA 360

EP 0 819 758 A2

CATGCTCATG GATACATCCC TGCCAAATTT CCAAGCAAGA ACCTGAAGAT GAATTATTGC 420
 CACAACCCCTG ACGGGGAGCC AAGGCCCTGG TGCTTCACAA CAGACCCAC CAAACGCTGG 480
 GAATACTGTG ACATCCCCCG CTGCACAACA CCCCCGCCCC CACCCAGCCC AACCTACCAA 540
 TGTCTGAAAG GAAGAGGTGA AAATTACCGA GGGACCGTGT CTGTCACCGT GTCTGGGAAA 600
 ACCTGTGAGC GCTGGAGTGA GCAAACCCCT CATAGGTGAG TCGAC 645

(2) INFORMATION FOR SEQ ID NO: 23:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Met Val Tyr Leu Ser Glu Cys Lys Thr Gly Ile Gly Asn Gly Tyr Arg
 1 5 10 15
 Gly Thr Met Ser Arg Thr Lys Ser Gly Val Ala Cys Gln Lys Trp Gly
 20 25 30
 Ala Thr Phe Pro His Val Pro Asn Tyr Ser Pro Ser Thr His Pro Asn
 35 40 45
 Glu Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Glu Gln
 50 55 60
 Gly Pro Trp Cys Tyr Thr Thr Asp Pro Asp Lys Arg Tyr Asp Tyr Cys
 65 70 75 80
 Asn Ile Pro Glu Cys Glu Glu Glu Cys Met Tyr Cys Ser Gly Glu Lys
 85 90 95
 Tyr Glu Gly Lys Ile Ser Lys Thr Met Ser Gly Lys Asp Cys Gln Ala
 100 105 110
 Trp Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ala Lys Phe
 115 120 125
 Pro Ser Lys Asn Leu Lys Met Asn Tyr Cys His Asn Pro Asp Gly Glu
 130 135 140
 Pro Arg Pro Trp Cys Phe Thr Thr Asp Pro Thr Lys Arg Trp Glu Tyr
 145 150 155 160
 Cys Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Pro Ser Pro Thr
 165 170 175

EP 0 819 758 A2

Tyr Gln Cys Leu Lys Gly Arg Gly Glu Asn Tyr Arg Gly Thr Val Ser
 180 185 190
 5 Val Thr Val Ser Gly Lys Thr Cys Gln Arg Trp Ser Glu Gln Thr Pro
 195 200 205
 His Arg His Asn Arg Thr Pro Glu Asn Phe Pro Cys Arg Asn Leu Glu
 210 215 220
 10 Glu Asn Tyr Cys Arg Asn Pro Asp Gly Glu Thr Ala Pro Trp Cys Tyr
 225 230 235 240
 Thr Thr Asp Ser Gln Leu Arg Trp Glu Tyr Cys Glu Ile Pro Ser Cys
 245 250 255
 15 Glu Ser Ser Ala Ser Pro Asp Gln Ser Asp Ser Ser Val Pro Pro Glu
 260 265 270
 Glu Gln Thr Pro Val Val Gln Glu Cys Tyr Gln Ser Asp Gly Gln Ser
 275 280 285
 Tyr Arg Gly Thr Ser Ser Thr Thr Ile Thr Gly Lys Lys Cys Gln Ser
 290 295 300
 25 Glu Gln Thr Pro His Arg Gly Lys Ser Met Val Tyr Leu Ser Glu Cys
 305 310 315 320
 Lys Thr Gly Ile Gly Asn Gly Tyr Arg Gly Thr Met Ser Arg Thr Lys
 325 330 335
 30 Ser Gly Val Ala Cys Gln Lys Trp Gly Ala Thr Phe Pro His Val Pro
 340 345 350
 Asn Tyr Ser Pro Ser Thr His Pro Asn Glu Gly Leu Glu Glu Asn Tyr
 355 360 365
 35 Cys Arg Asn Pro Asp Asn Asp Glu Gln Gly Pro Trp Cys Tyr Thr Thr
 370 375 380
 Asp Pro Asp Lys Arg Tyr Asp Tyr Cys Asn Ile Pro Glu Cys Glu Glu
 385 390 395 400
 40 Glu Cys Met Tyr Cys Ser Gly Glu Lys Tyr Glu Gly Lys Ile Ser Lys
 405 410 415
 Thr Met Ser Gly Lys Asp Cys Gln Ala Trp Asp Ser Gln Ser Pro His
 420 425 430
 45 Ala His Gly Tyr Ile Pro Ala Lys Phe Pro Ser Lys Asn Leu Lys Met
 435 440 445
 Asn Tyr Cys His Asn Pro Asp Gly Glu Pro Arg Pro Trp Cys Phe Thr
 450 455 460
 50 Thr Asp Pro Thr Lys Arg Trp Glu Tyr Cys Asp Ile Pro Arg Cys Thr
 55

EP 0 819 758 A2

	465		470		475		480									
8	Thr	Pro	Pro	Pro	Pro	Ser	Pro	Thr	Tyr	Gln	Cys	Leu	Lys	Gly	Arg	
				485					490					495		
	Gly	Glu	Asn	Tyr	Arg	Gly	Thr	Val	Ser	Val	Thr	Val	Ser	Gly	Lys	Thr
			500					505					510			
10	Cys	Gln	Arg	Trp	Ser	Glu	Gln	Thr	Pro	His	Arg	His	Asn	Arg	Thr	Pro
			515					520					525			
	Glu	Asn	Phe	Pro	Cys	Arg	Asn	Leu	Glu	Glu	Asn	Tyr	Cys	Arg	Asn	Pro
		530					535					540				
15	Asp	Gly	Glu	Thr	Ala	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Ser	Gln	Leu	Arg
	545				550					555						560
	Trp	Glu	Tyr	Cys	Glu	Ile	Pro	Ser	Cys	Glu	Ser	Ser	Ala	Ser	Pro	Asp
				565						570					575	
20	Gln	Ser	Asp	Ser	Ser	Val	Pro	Pro	Glu	Glu	Gln	Thr	Pro	Val	Val	Gln
			580						585					590		
	Glu	Cys	Tyr	Gln	Ser	Asp	Gly	Gln	Ser	Tyr	Arg	Gly	Thr	Ser	Ser	Thr
		595					600						605			
25	Thr	Ile	Thr	Gly	Lys	Lys	Cys	Gln	Ser	Glu	Gln	Thr	Pro	His	Arg	
		610					615					620				

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1284 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

60	GTCGACATGG TGTATCTGTC AGAATGTAAG ACCGGCATCG GCAACGGCTA CAGAGGAACC
120	ATGTCCAGGA CAAAGAGTGG TGTTCCTGT CAAAAGTGGG GTGCCACGTT CCCCCACGTA
180	CCCAACTACT CTCCAGTAC ACATCCCAAT GAGGGACTAG AAGAGAACTA CTGTAGGAAC
240	CCAGACAATG ATGAACAAGG GCCTTGGTGC TACTACTACG ATCCGGACAA GAGATATGAC
300	TACTGCAACA TTCCTGAATG TGAAGAGGAA TGCATGTACT GCAGTGGAGA AAAGTATGAG
360	GGCAAAATCT CCAGACCAT GTCTGGACTT GACTGCCAGG CCTGGGATTC TCAGAGCCCA

EP 0 819 758 A2

CATGCTCATG GATACATCCC TGCCAAATTT CCAAGCAAGA ACCTGAAGAT GAATTATTGC 420
 CACAACCCCTG ACGGGGAGCC AAGGCCCTGG TGCTTCACAA CAGACCCAC CAAACGCTGG 480
 GAATACTGTG ACATCCCCCG CTGCACAACA CCCCCGCCCC CACCCAGCCC AACCTACCAA 540
 TGTCTGAAAG GAAGAGGTGA AAATTACCGA GGGACCGTGT CTGTCACCGT GTCTGGGAAA 600
 ACCTGTCAGC GCTGGAGTGA GCAAACCCCT CATAGGGGTA AAAGAATGGT GTATCTGTCA 660
 GAATGTAAGA CCGGCATCGG CAACGGCTAC AGAGGAACCA TGTCCAGGAC AAAGAGTGGT 720
 GTTGCTGTG AAAAGTGGG TGCCACGTC CCCCACGTAC CCAACTACTC TCCAGTACA 780
 CATCCCAATG AGGGACTAGA AGAGAACTAC TGTAGGAACC CAGACAATGA TGAACAAGGG 840
 CCTTGGTGCT ACACTACAGA TCCGGACAAG AGATATGACT ACTGCAACAT TCCTGAATGT 900
 GAAGAGGAAT GCATGTACTG CAGTGGAGAA AAGTATGAGG GCAAAATCTC CAAGACCATG 960
 TCTGGACTTG ACTGCCAGGC CTGGGATTCT CAGAGCCAC ATGCTCATEG ATACATCCCT 1020
 GCCAAATTC CAAGCAAGAA CTTGAAGATG AATTATTGCC ACAACCCTGA CGGGGAGCCA 1080
 AGGCCCTGGT GCTTCACAAC AGACCCACC AAACGCTGGG AATACTGTGA CATCCCCCGC 1140
 TGCACAACAC CCCCCCCCC ACCCAGCCCA ACCTACCAAT GTCTGAAGG AAGAGGTGAA 1200
 AATTACCGAG GGACCGTGTG TGTACCGTG TCTGGGAAA CCTGTCAGCG CTGGAGTGAG 1260
 CAAACCCCTC ATAGGTGAGT CGAC 1284

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Met Leu Pro Ile Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu
 1 5 10 15
 Arg Glu Leu Phe Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn
 20 25 30
 Leu Ser Ser Glu Met Phe Ser Glu Phe Glu Lys Arg Tyr Thr His Gly
 35 40 45
 Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu
 50 55 60

EP 0 819 758 A2

Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
65 70 75 80

Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
85 90 95

Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Gln Ala
100 105 110

Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys
115 120 125

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GTGACATGT TGCCATCTG TCCCGGCGG GCTGCCCGAT GCCAGGTGAC CCTTCGAGAC 60

CTGTTTGACC GCGCGTCTGT CCGTCCAC TACATCCATA ACCTCTCCTC AGAAATGTTT 120

AGCGAATTCG ATAAACGGTA TACCCATGGC CGGGGGTTCA TTACCAAGGC CATCAACAGC 180

TGCCACACTT CTTCCCTTGC CACCCCCGAA GACAAGGAGC AAGCCCAACA GATGAATCAA 240

AAAGACTTTC TGAGCCTGAT AGTCAGCATA TTGCGATCCT GGAATGAGCC TCTGTATCAT 300

CTGGTCACGG AAGTACGTGG TATGCRAGAA GCCCCGGAGG CTATCCTATC CAAAGCTGTA 360

GAGATTGAGG AGCAAACCTA AGTCGAC 387

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

EP 0 819 758 A2

Met Leu Pro Ile Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu
1 5 10 15

Arg Glu Leu Phe Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn
20 25 30

Leu Ser Ser Glu Met Phe Ser Glu Phe Glu Lys Arg Tyr Thr His Gly
35 40 45

Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu
50 55 60

Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
65 70 75 80

Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
85 90 95

Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Gln Ala
100 105 110

Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys Gly Lys Ser
115 120 125

Met Leu Pro Ile Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu
130 135 140

Arg Glu Leu Phe Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn
145 150 155 160

Leu Ser Ser Glu Met Phe Ser Glu Phe Glu Lys Arg Tyr Thr His Gly
165 170 175

Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu
180 185 190

Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
195 200 205

Phe Leu Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu
210 215 220

Pro Leu Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro
225 230 235 240

Gln Ala Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys
245 250 255

(2) INFORMATION FOR SEQ ID NO: 28:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

ATGTTGCCCA TCTGTCCCGG CGGGGCTGCC CGATGCCAGG TGACCCCTTCG AGACCTGTTT 60
 GACCGCGCCG TCGTCCTGTC CCACTACATC CATAACCTCT CCTCAGAAAT GTTCAGCGAA 120
 TTCGATAAAC GGTATACCCA TGGCGGGGGG TTCATTACCA AGGCCATCAA CAGCTGCCAC 180
 ACTTCTTCCC TTGCCACCCC CGAAGACAAG GAGCAAGCCC AACAGATGAA TCAAAAAGAC 240
 TTCTGAGCC TGATAGTCAG CATATTGCGA TCCTGGAATG AGCCTCTGTA TCATCTGGTC 300
 ACGGAAGTAC GTGGTATGCA AGAAGCCCCG GAGGCTATCC TATCCAAGC TGTAGAGATT 360
 GAGGAGCAAA CCGGTAAAAG AATGTTGCCC ATCTGTCCCG GCGGGGCTGC CCGATGCCAG 420
 GTGACCCCTC GAGACCTGTT TGACCGCGCC GTCGTCTGT CCCACTACAT CCATAACCTC 480
 TCCTCAGAAA TGTTCAGCGA ATTCGATAAA CGGTATACCC ATGGCCGGGG GTTCATTACC 540
 AAGGCCATCA ACAGCTGCCA CACTTCTTCC CTGCCCACCC CCGAAGACAA GGAGCAAGCC 600
 CAACAGATGA ATCAAAAAGA CTTTCTGAGC CTGATAGTCA GCATATTGCG ATCCTGGAAT 660
 GAGCCTCTGT ATCATCTGGT CACGGAAGTA CGTGGTATGC AAGAAGCCCC GGAGGCTATC 720
 CTATCCAAAG CTGTAGAGAT TGAGGAGCAA ACCTAA 756

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ATGCTGAGGC GGCCTCCCCCT ATGCTATCAC AACGGAGTTC AGTACAGAAA TAACGGTAAA 60
 AGATCCCCGT GGTTCATCTTG TTCTGTGACA TGTGGTGATG GTGTGATGTT AAAAGAAGTG 120
 GTACCCCTGTA GACAAGACAG TGGACACCTC CTCCCCATTA A 161

(2) INFORMATION FOR SEQ ID NO: 30:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met Leu Arg Arg Pro Pro Leu Cys Tyr His Asn Gly Val Gln Tyr Arg
 1 5 10 15
 Asn Asn Glu Glu Trp Thr Val Asp Ser Gly Lys Ser Ser Pro Trp Ser
 20 25 30
 Ser Cys Ser Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Gly Lys
 35 40 45
 Ser Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly Val
 50 55 60

(2) INFORMATION FOR SEQ ID NO: 31:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATGCTGAGGC GGCCTCCCCT ATGCTATCAC AACGGAGTTC AGTACAGAAA TAACCGTAAA 60
 AGATCCCCGT GGTCACTCTG TTCTGTGACA TGTGTTGATG GTGTGATGTT AAAAGAAGTG 120
 GTACCCCTGTA GACAAGACAG TGGACACCTC CTCGCCATTA TATTGGTTCT CGTGGTAAAA 180
 GATAA 185

(2) INFORMATION FOR SEQ ID NO: 32:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

TAGGTCTAGA ATGACTGAAG AGAACAAAGA G

31

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

ATGGTCTAGA TTAGAGACGA CTACGTTTCT G

31

Claims

1. A cationic liposome:DNA complex comprising DNA encoding an anti-angiogenic peptide.
2. A cationic polymer:DNA complex comprising the DNA encoding an antiangiogenic peptide.
3. The complex of Claim 1, wherein said complex additionally comprises DNA encoding a tumor suppressor protein.
4. The complex of Claim 2, wherein said complex additionally comprises DNA encoding a tumor suppressor protein.
5. The complex of Claim 1, wherein said cationic liposomes are comprised of one cationic lipid (i.e., 1,2-dioleoyl-sn-glycero-3-ethylphosphocholine, 1,2-dimyristoyl-sn-glycero-3-ethylphosphocholine, and 2,3-dioleoylpropyl-N,N,N-trimethyl-ammonium chloride) and may also be comprised of polyethylene glycol (i.e., a pegylated lipid-1,2-diacyl-sn-glycero-3-phospho-ethanolamine-N-Poly(ethylene glycol) 2000) and a targeted ligand (the amino acid peptide RGD, ferritin, or antibodies targeted toward to HER2).
6. The complex of Claim 1, wherein said cationic liposomes are comprised of one cationic polymer polyethylenimine Polycat57, polylysine, polyhistidine, and Superfect) and may also be comprised of polyethylene glycol and a targeted ligand (the amino acid peptide RGD, ferritin, or antibodies targeted toward to HER2, CEA).
7. The complex of Claims 4 or 5, wherein said tumor suppressor protein is selected from the group consisting of the p53, the p21 and the rb.
8. The complex of Claims 3 or 4, wherein said tumor suppressor protein is p53.
9. The complex of Claims 1, 2, or 3, wherein said anti-angiogenic peptide is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID

NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, and SEQ ID NO:30.

10. The complex of Claims 1 or 3, wherein said DNA encoding an anti-angiogenic peptide is present in an amount of from 0.0025 to 0.16 $\mu\text{g}/\mu\text{M}$ of liposome.
11. The complex of Claims 2 or 4, wherein said DNA encoding an anti-angiogenic peptide is present in an amount of from 0.016 to 0.33 $\mu\text{g}/\mu\text{g}$ of polymer.
12. The complex of Claim 8, wherein said DNA encoding a tumor suppressor protein is present in an amount of from 0.0025 to 0.16 $\mu\text{g}/\mu\text{M}$.
13. The complex of Claim 8, wherein said DNA encoding a tumor suppressor protein is present in an amount of from 0.016 to 0.33 $\mu\text{g}/\mu\text{M}$.
14. Use of a cationic polymer:DNA complex comprising DNA encoding an anti-angiogenic peptide for the production of a medicament for inhibiting tumor growth in a subject which preferably comprises administering the same to a tumor-bearing subject.
15. The use of Claim 14, where said complex additionally comprises DNA encoding a tumor suppressor protein.
16. The use of claim 1, wherein said cationic liposome (i.e., 1,2-dioleoyl-sn-glycero-3-ethylphosphocholine, 1,2-dimyristoyl-sn-glycero-3-ethylphosphocholine, and 2,3-di(1-oxy)propyl-N,N,N-trimethylammonium chloride and may also be comprised of polyethylene glycol (i.e., a pegylated lipid-1,2-diacy-sn-glycero-3-phospho-ethanolamine-N-[Poly-(ethylene glycol) 2000] and a targeted ligand (the amino acid peptide RGD, ferritin, or antibodies targeted toward to HER2).
17. The use of claim 2, wherein said cationic polymer (i.e. (polyethylenimine Polycat57, polylysine, polyhistidine, and Superfect) and may also be comprised of polyethylene glycol and a targeted ligand (the amino acid peptide RGD, ferritin, or antibodies targeted toward to HER2).
18. The use of Claim 15, wherein said tumor suppressor protein is selected from the group consisting of p53, the p21 and the rb.
19. The use of Claim 18, wherein said tumor suppressor protein is p53.
20. The use of Claim 14, wherein said anti-angiogenic peptide is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, and SEQ ID NO:30.
21. The use of Claim 14 or Claim 15, wherein said DNA encoding an anti-angiogenic peptide is present in an amount from 0.0025 to 0.16 $\mu\text{g}/\mu\text{M}$ of liposome or 0.016 to 0.33 $\mu\text{g}/\mu\text{g}$ of polymer.
22. The use of Claims 14 or 15, wherein said DNA encoding a tumor suppressor protein is present in an amount of from 0.0025 to 0.16 $\mu\text{g}/\mu\text{M}$ of liposome or 0.016 to 0.33 $\mu\text{g}/\mu\text{g}$ of polymer.
23. A cationic polymer:DNA complex comprising a plasmid with one or more promoters expressing either the same gene product (SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, and SEQ ID NO:30) or combinations of these gene products.
24. A cationic liposome:DNA complex comprising a plasmid with an intervening internal ribosomal entry site sequence between two genes (SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, and SEQ ID NO:29) that are either the same or different.
25. The complex of Claim 1 or Claim 2, wherein said anti-angiogenic protein is secretory from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID

EP 0 619 758 A2

NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, and SEQ ID NO:30.

5

10

15

20

25

30

35

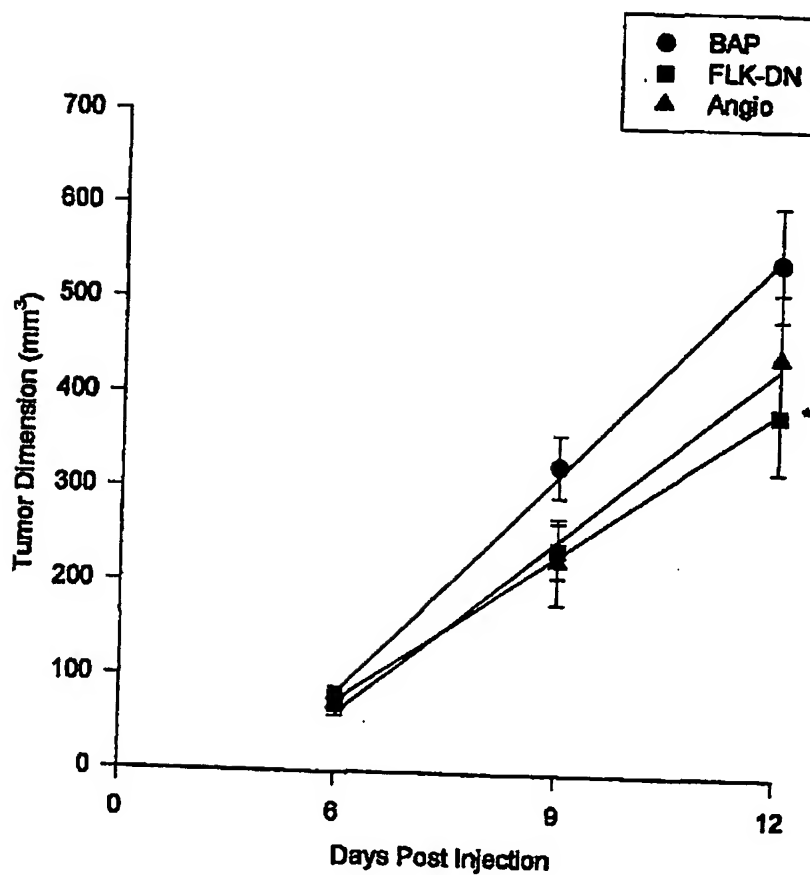
40

45

50

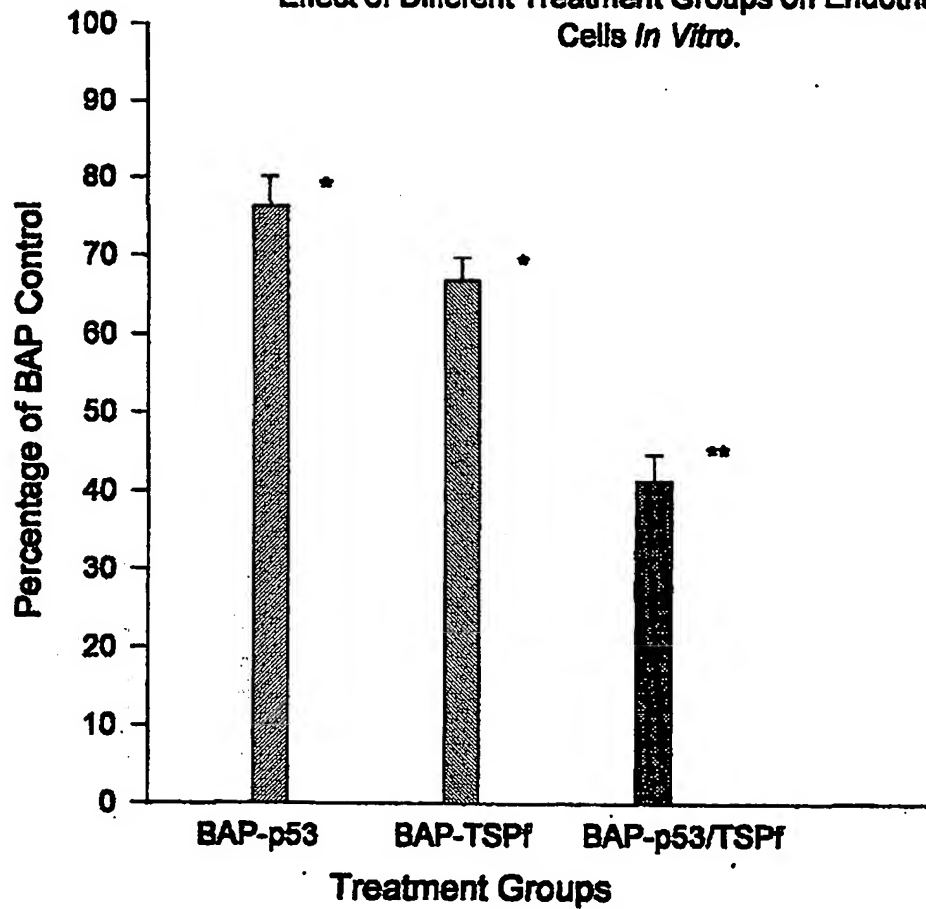
55

Figure 1
Intratumoral Injections of Liposome:DNA Complexes



*, Angio vs. BAP, $p < 0.05$

Figure 2
Effect of Different Treatment Groups on Endothelial
Cells *In Vitro*.



*- BAP vs BAP-p53 or BAP-TSPf, $p < 0.05$

** - BAP-p53 or BAP-TSPf vs BAP-p53/BAP-TSPf, $p < 0.01$

THIS PAGE BLANK (USPTO)

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☒ **BLACK BORDERS**
- ☒ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- ☒ **FADED TEXT OR DRAWING**
- ☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
- ☒ **LINES OR MARKS ON ORIGINAL DOCUMENT**
- ☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- ☐ **OTHER:** _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.

THIS PAGE BLANK (USPTO)